

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 18.2546 Seconds
(without alignments)
716.207 Million cell updates/sec

Title: US-10-052-798-9

Perfect score: 1633
Sequence: 1 MTMTSPSGAFLEIFNVK.....HHGGAEOKISEDLNGAA 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Dackfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	1633	100.0	309	4	US-09-079-029-9
2	1460.5	89.4	312	4	US-09-079-029-10
3	1231.5	75.4	310	4	US-09-079-029-11
4	1155	70.7	280	3	US-09-260-527-1
5	1010	61.8	278	3	US-09-260-527-3
6	923.5	56.6	249	4	US-10-039-785-53
7	871	53.3	284	3	US-09-184-638-40
8	838.5	51.3	289	3	US-09-184-658-63
9	825	50.5	297	4	US-09-486-814A-2
10	811	49.7	334	4	US-09-646-028-53
11	811	49.7	339	4	US-09-646-028-55
12	805	49.3	348	4	US-09-646-028-51
13	804	49.2	284	3	US-08-564-164A-2
14	785.5	48.1	245	4	US-08-918-148-75
15	783.5	48.0	245	4	US-08-918-148-76
16	776.5	47.6	282	2	US-08-860-174A-10
17	767.5	47.0	255	4	US-09-553-498-8
18	767.5	47.0	255	4	US-09-618-868-8
19	764.5	46.8	245	4	US-08-918-148-78
20	764	46.8	244	4	US-08-918-148-77
21	762	46.7	301	2	US-08-661-052-14
22	762	46.7	301	3	US-09-188-082-14
23	762	46.7	301	4	US-09-364-088-14
24	762	46.7	301	4	US-09-102-716-14
25	759.5	46.5	240	1	US-08-488-113B-148
26	759.5	46.5	240	1	US-08-477-484B-148
27	759.5	46.5	240	2	US-08-646-360-148

28	759.5	46.5	240	3	US-08-839-765-148	Sequence 148, App
29	759.5	46.5	240	3	US-09-136-389-148	Sequence 148, App
30	759.5	46.5	240	4	US-09-610-838-148	Sequence 148, App
31	749.5	45.9	281	4	US-09-025-769B-178	Sequence 178, App
32	744.5	45.6	245	4	US-10-039-785-42	Sequence 42, App
33	741.5	45.4	359	4	US-09-646-028-16	Sequence 16, App
34	737	45.1	244	4	US-08-918-148-79	Sequence 79, App
35	735.5	45.0	361	4	US-09-646-028-13	Sequence 13, App
36	732	44.8	277	2	US-08-256-790-2	Sequence 2, App
37	728.5	44.6	245	4	US-10-039-785-48	Sequence 48, App
38	728	44.6	267	4	US-09-485-737B-2	Sequence 2, App
39	723.5	44.3	249	4	US-08-918-148-74	Sequence 74, App
40	721.5	44.2	245	4	US-10-039-785-43	Sequence 43, App
41	720.5	44.1	245	4	US-10-039-785-49	Sequence 49, App
42	719	44.0	268	4	US-09-554-765-2	Sequence 2, App
43	716.5	43.9	258	2	US-08-665-202-5	Sequence 5, App
44	716.5	43.9	258	4	US-09-315-574-5	Sequence 5, App
45	712.5	43.6	245	4	US-10-039-785-46	Sequence 46, App

ALIGNMENTS

RESULT 1
US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntarapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-079-029-9
Query Match 100.0%; Score 1633; DB 4; Length 309;
Best local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTMTSPSGAFLEIFNVKLLFAIPLVVPEFAAOPMAEVOYVGSGGVERGSLRS 60
|||||
DB 1 MTMTSPSGAFLEIFNVKLLFAIPLVVPEFAAOPMAEVOYVGSGGVERGSLRS 60
QY 61 CAASGFTPDYGSWVRQAPGKGLIEWVSGINNGSGTGYADSVKGRVTTISRDNAKNSLYL 120

```
Db 61 CAASGTFDDYGSWYRQAPGKLEWVSGINMNGSGTYADSVKGRFTTISRDAKNSLYL 120
QY 121 QMNSLRAEDTAVYYCAKIIAGAGRWYFDLMGKGTVTYSSGGSGSGGSGGSSSELTQ 180
Db 121 QMNSLRAEDTAVYYCAKIIAGAGRWYFDLMGKGTVTYSSGGSGSGGSGGSSSELTQ 180
QY 181 DPAVSVALQGVTRITCGDSLRSYASWYQKPGQAPVLYTGKNNRPSGIDPREFSGSS 240
Db 181 DPAVSVALQGVTRITCGDSLRSYASWYQKPGQAPVLYTGKNNRPSGIDPREFSGSS 240
QY 241 GMTASLTITGAQAEDEADYCNRSRSGNHVYFGGCTKLTVLGAANHNNHNGAAEQKLI 300
Db 241 GMTASLTITGAQAEDEADYCNRSRSGNHVYFGGCTKLTVLGAANHNNHNGAAEQKLI 300
QY 301 SEEDLINGAA 309
Db 301 SEEDLINGAA 309
```

RESULT 2

```
US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-10
```

```
Query Match 89.4%; Score 1460.5; DB 4; Length 312;
Best Local Similarity 90.1%; Pred. No. 5.1e-107;
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;
```

```
QY 1 MTMTSPGAFLEIFNVKLLFAIPLVVFYAQAQPMAMAEVOLVQSGGGERGSLRLS 60
Db 1 MTMTSPGAFLEIFNVKLLFAIPLVVFYAQAQPMAMAEVOLVQSGGGERGSLRLS 60
QY 61 CAASGTFDDYGSWYRQAPGKLEWVSGINMNGSGTYADSVKGRFTTISRDAKNSLYL 120
Db 61 CAASGTFSSYMWSWRQAPGKLEWVANIKDGSSEKYYDSVKGRFTISRDAKNSLYL 120
```

```
QY 121 QMNSLRAEDTAVYYCA-----KIIAGAGRWYFDLMGKGTVTYSSGGSGSGGSGGSS 176
Db 121 QMNSLRAEDTAVYYCARDLLKVKGSSSGW-FDEWGRGTTVTYSSGGSGSGGSGGSS 179
QY 177 ELTQDPAVSVALQGVTRITCGDSLRSYASWYQKPGQAPVLYTGKNNRPSGIDPREFS 236
Db 180 ELTQDPAVSVALQGVTRITCGDSLRSYASWYQKPGQAPVLYTGKNNRPSGIDPREFS 239
QY 237 GSSSGMTASLTITGAQAEDEADYCNRSRSGNHVYFGGCTKLTVLGAANHNNHNGAAE 296
Db 240 GSSSGMTASLTITGAQAEDEADYCNRSRSGNHVYFGGCTKLTVLGAANHNNHNGAAE 299
QY 297 QKLISEEDLINGAA 309
Db 300 QKLISEEDLINGAA 312
```

RESULT 3

```
US-09-079-029-11
; Sequence 11, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-11
```

```
Query Match 75.4%; Score 1231.5; DB 4; Length 310;
Best Local Similarity 78.0%; Pred. No. 4.4e-69;
Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;
```

```
QY 1 MTMTSPGAFLEIFNVKLLFAIPLVVFYAQAQPMAMAEVOLVQSGGGERGSLRLS 60
Db 1 MTMTSPGAFLEIFNVKLLFAIPLVVFYAQAQPMAMAEVOLVQSGGGERGSLRLS 60
QY 61 CAASGTFDDYGSWYRQAPGKLEWVSGINMNGSGTYADSVKGRFTTISRDAKNSLYL 120
Db 61 CAASGTFSSYGHVHWYRQAPGKLEWVAGIFDGNKYYADSVKGRFTTISRDAKNSLYL 120
QY 121 QMNSLRAEDTAVYYCAKIIAGAGRWYFDLMGKGTVTYSSGGSGSGGSGGSSSELTQ 178
Db 121 QMNSLRAEDTAVYCAR-----DRGYIMYWGKGTITVTYSSGGSGSGGSGGSSQSYL 176
```

```
QY 179 TQDPAYVALGOTVIRITCGDSLRL---SYASWYQOKPGQAPVLYTYGKNNRPSGIPDRF 235
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      177 TQDPVSGAPGQVIRITCGSSNNICAGHDVHWYQQLPQTAKKLIIYDSSNRPSPGPRDF 236
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      QY 236 SSSSSGNTASLTITGAQAEDEADYCNRSRDSGNNHVFQGGTKLVLGAAHHHHHNGAA 295
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      Db 237 SGRSGTSASLTITGLQAEDEADYCCOSYDSSLRGSVFQGGTKVTVLGAAHHHHHNGAA 296
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      QY 296 EOKLISEEDLNGAA 309
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      Db 297 EOKLISEEDLNGAA 310
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 4

```
US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J. P.
; APPLICANT: Mikkelson, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DY0019.001AUS
; CURRENT APPLICATION NUMBER: US/09/260.527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PRP
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
; OTHER INFORMATION: phage display library known as the Synthetic scfv
; OTHER INFORMATION: Library (#1) from the Centre for Protein
; OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
US-09-260-527-1
```

Query Match

Best Local Similarity 82.9%; Score 1155; DB 3; Length 280;
Matches 232; Conservative 11; Mismatches 19; Indels 18; Gaps 4;

```
QY 33 AAOPMAEYQVQSGGVERPGSGRLSCAAGTFEDDYG-MSWYRQAPKGLEWYSGI-- 90
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      Db 16 AAOPMAEYQVQSGGVERPGSGRLSCAAGTFEDDYG-MSWYRQAPKGLEWYSGI-- 75
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      QY 91 MNNGSTGYADSVKGRVTISRDNKNSLYLQNSLRAEDTAVYYCAKILGAGRWYFDL- 149
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      Db 76 KTDGCTDYAAPVKGKRFITSRDSSKNTLYLQNSLKTEDTAVYYCA-----RKNRKALR 129
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      QY 150 WCKGTTVYSSGGGSGGGGSSSELTQDPAYVALGOTVIRITCGDSLRSYASWY 209
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      Db 130 WQGGTLVYSSRGGGSGGGGSSSELTQDPAYVALGOTVIRITCGDSLRSYASWY 189
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      QY 210 QOKPGQAPVLYTYGKNNRPSGIPDRFSSGSGNTASLTITGAQAEDEADYCNRSRDSGN 269
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      Db 190 QOKPGQAPVLYTYGKNNRPSGIPDRFSSGSGNTASLTITGAQAEDEADYCNRSRDSGN 249
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      QY 270 HVFQGGTKLVLGAAHHHHHNGAAEOKLISEEDLNGAA 309
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      Db 250 HVFQGGTKLVLGAA-----AAEOKLISEEDLNGAA 280
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 5

```
US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J. P.
; APPLICANT: Mikkelson, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
```

```
; FILE REFERENCE: DY0019.001AUS
; CURRENT APPLICATION NUMBER: US/09/260.527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 278
; TYPE: PRP
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
; OTHER INFORMATION: from a naive phage display library known as the
; OTHER INFORMATION: Synthetic scfv library (#1) from the Centre for
; OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3
```

Query Match

Best Local Similarity 61.8%; Score 1010; DB 3; Length 278;
Matches 204; Conservative 21; Mismatches 37; Indels 16; Gaps 5;

```
QY 33 AAOPMAEYQVQSGGVERPGSGRLSCAAGTFEDDYG-MSWYRQAPKGLEWYSGIN 91
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      Db 16 AAOPMAEYQVQSGGVERPGSGRLSCAAGTFEDDYG-MSWYRQAPKGLEWYSGIN 74
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      QY 92 MNNGSTGYADSVKGRVTISRDNKNSLYLQNSLRAEDTAVYYCAKILGAGRWYFDLNG 151
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      Db 75 YSSGTYVYVNSLKSRYTMSVDTSKNOFSLKSSVTAADVAYVCARF-----HPRVYD-WG 129
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      QY 152 KGTIVYSSGGGSGGGGSSSELTQDPAYVALGOTVIRITCGDSLRSYASWYQ 211
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      Db 130 QGTIVYSSRGGGSGGGGSSSELTQDPAYVALGOTVIRITCGDSLRSYASWYQ 189
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      QY 212 KPGQAPVLYTYGKNNRPSGIPDRFSSGSGNTASLTITGAQAEDEADYCNRSRDSGNV 271
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      Db 190 KPGQAPVLYTYGKNNRPSGIPDRFSSGSGNTASLTITGAQAEDEADYCNRSRDSGNV 249
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      QY 272 VFGGTKLVLGAAHHHHHNGAAEOKLISEEDLNGAA 309
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      Db 250 VFGGTKLVLGAA-----AAEOKLISEEDLNGAA 278
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 6

```
US-10-039-785-53
; Sequence 53, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039.785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
```

```

Patent No. 6030792
GENERAL INFORMATION:
APPLICANT: O'Brien, Ivan G.
APPLICANT: Mezes, Peter S.
APPLICANT: Downs, James T.
APPLICANT: Johnson, Kimberly S.
TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
FILE REFERENCE: PC9946-A
CURRENT APPLICATION NUMBER: US/09/184,658
EARLIER APPLICATION NUMBER: 60/065,423
EARLIER FILING DATE: 1997-11-13
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 40
LENGTH: 284
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 9A4 scFv VH -
OTHER INFORMATION: VL.
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)..(22)
OTHER INFORMATION: pCANTAB6 signal peptide; Val at position 1 is most
OTHER INFORMATION: likely the initiator Met.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (23)..(137)
OTHER INFORMATION: 9A4 VH domain.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (138)..(152)
OTHER INFORMATION: 15 amino acid linker.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (153)..(258)

```

```

RESULT 8
US-09-184-658-63
: Sequence 63, Application US/09184658
: Patent No. 6030792
: GENERAL INFORMATION:
: APPLICANT: Oltmanns, Ivan G.
: APPLICANT: Mezes, Peter S.
: APPLICANT: Downs, James T.
: APPLICANT: Johnson, Kimberly S.
: TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
: TITLE OF INVENTION: Bioloigical Media
: FILE REFERENCE: PC9946-A
: CURRENT APPLICATION NUMBER: US/09/184,658
: CURRENT FILING DATE: 1998-11-02
: EARLIER APPLICATION NUMBER: 60/065,423
: EARLIER FILING DATE: 1997-11-13
: NUMBER OF SEQ ID NOS: 69
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 63
: LENGTH: 289
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL
: OTHER INFORMATION: scfv.
: FEATURE:
: NAME/KEY: SIGNAL
: LOCATION: (1)..(22)
: OTHER INFORMATION: pcANTAB6 signal peptide; Val at position 1 is most
: OTHER INFORMATION: likely Initiator Met.
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (23)..(138)
: OTHER INFORMATION: 5109 VH domain.
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (139)..(154)

```


OTHER INFORMATION: Identification Method: P

200 SSGNHVFEGGGKLVLDGAAADNNNNN 292
| : ||||| | | |||||

Db 311 DSLSGWLFGGGTLVTLV---RHNNHHH 334

RESULT 11

US-09-646-028-55

Sequence 55, Application US/09646028

Patent No. 6562347

GENERAL INFORMATION:

APPLICANT: Kwak, Larry

APPLICANT: Biragyn, Atya

TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES

FILE REFERENCE: 14014.0316/P

CURRENT APPLICATION NUMBER: US/09/646,028

PRIOR FILING DATE: 2000-09-12

PRIOR APPLICATION NUMBER: 60/077,745

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 55

LENGTH: 339

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct.

US-09-646-028-55

Query Match

Best Local Similarity 49.7%; Score 811; DB 4; Length 339;

Best Local Similarity 61.0%; Pred. No. 4,1e-56;

Matches 163; Conservative 28; Mismatches 64; Indels 12; Gaps 5;

QY 33 AAOPAAAEVQVVOGSGGVERPGGSLRLSCAASGFTTFDDYGMGMSVRQAPKGLWVSGIMNW 92

Db 78 AQAAPKSLVEQLLESGLVQSGGSLRLSCVAGSLTFPSSAIIWVRQAPKGLWVSGISF 137

QY 93 NGSGCYADSVKGRVYISPDNAKNSLYLQMSLRADTVAYVYCAKILGAGRGVYFPLMK 152

Db 138 SDDTYVADSVKGRFSASDNSKNVYLLQMNILRPDVAVYFCAN--NOTGNFCLDNWQ 195

QY 153 GTTVVSS-GGGSGGGSGGGSGGS--SETLQDPVAVSALQGVTRITCOGDSLR--SY 205

Db 196 GTLVTVSSKSGGSGGGSGGSQSVLTQPPVSAPAGQVITISCGSSNIGAGVD 255

QY 206 ASWYQKRGQAPVLYLYGNRPSCIPDRFSGSSSGNTASLTITGAQADEADYCNSSRD 265

Db 256 VMWYKRFETAPKAVLYISNNRPSGVPRFSGSGSASLAITGLQLEDEGTYCOCMD 315

QY 266 SSGNHVVRGGGTRKLVTLVGAHHHHH 292

Db 316 DSLSGWLFGGGTLVTLV---RHNNHHH 339

RESULT 12

US-09-646-028-51

Sequence 51, Application US/09646028

Patent No. 6562347

GENERAL INFORMATION:

APPLICANT: Kwak, Larry

APPLICANT: Biragyn, Atya

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF

FILE REFERENCE: 14014.0316/P

CURRENT APPLICATION NUMBER: US/09/646,028

CURRENT FILING DATE: 2000-09-12

PRIOR APPLICATION NUMBER: 60/077,745

PRIOR FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 51

LENGTH: 348

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct

US-09-646-028-51

Query Match

Best Local Similarity 49.3%; Score 805; DB 4; Length 348;

Best Local Similarity 61.9%; Pred. No. 1,3e-55;

Matches 161; Conservative 28; Mismatches 59; Indels 12; Gaps 5;

QY 40 EVOLVOSGGGVERPGGSLRLSCAASGFTTFDDYGMGMSVRQAPKGLWVSGIMNWGSTGY 99

Db 94 EVOLLESGLVQSGGSLRLSCVAGSLTFPSSAIIWVRQAPKGLWVSGISFSGDTYV 153

QY 100 ADSVGRVYISPDNAKNSLYLQMSLRADTVAYVYCAKILGAGRGVYFPLMKRTVYVS 159

Db 154 ADSVGRFSASDNSKNVYLLQMNILRPDVAVYFCAN--NOTGNFCLDNWQGLTVTVS 211

QY 160 S-GGGSGGGSGGGSGGS--SETLQDPVAVSALQGVTRITCOGDSLR--SYASWYQK 212

Db 212 SRGGSGGGSGGGSGGSQSVLTQPPVSAPAGQVITISCGSSRNITAGDVWYQKF 271

QY 213 PGQAPVLYLYGNRPSCIPDRFSGSSSGNTASLTITGAQADEADYCNSSDSSGNHYV 272

Db 272 PETAPKVLIVYISNNRPSGVPRFSGSGSASLAITGLQLEDEGTYCOCMDDSLGLW 331

QY 273 FGGGTRKLVTLVGAHHHHH 292

Db 332 FGGGTRKLVTLV---RHNNHHH 348

RESULT 13

US-08-564-164A-2

Sequence 2, Application US/08564164A

Patent No. 6159947

GENERAL INFORMATION:

APPLICANT: Schweighofer, Fabien

APPLICANT: Tocque, Bruno

TITLE OF INVENTION: Intracellular Binding Proteins and Use

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Road, 3C43

CITY: Collegenville

STATE: PA

COUNTRY: USA

ZIP: 19426-0107

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/564,164A

FILING DATE: 28-DEC-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/FR94/00714

FILING DATE: 15-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 93/07241

FILING DATE: 16-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Savitsky, Marlin F.

REGISTRATION NUMBER: 29,699

REFERENCE/DOCKET NUMBER: ST93030-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610)454-3816

TELEFAX: (610)454-3808

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 284 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-564-164A-2

Query Match	49.28;	Score 804;	DB 3;	Length 284;
Best Local Similarity	59.88;	Pred. No. 1.2e-55;		
Matches 165;	Conservative 32;	Mismatches 65;	Indels 14;	Gaps 5;

[illegible]

RESULT 14

```

US-08-918-148-75
:
: Sequence 75, Application US/08918148A
: Patent No. 6342220
:
: GENERAL INFORMATION:
:
: APPLICANT: Adams, Camellia
:
: APPLICANT: W.
:
: APPLICANT: Carter, Paul J.
:
: APPLICANT: Fendly, Brian M.
:
: APPLICANT: Gurney, Austin L.
:
: TITLE OF INVENTION: Agonist Antibodies
:
: FILE REFERENCE: P0979
:
: CURRENT APPLICATION NUMBER: US/08/918,148A
:
: CURRENT FILING DATE: 1997-08-25
:
: NUMBER OF SEQ ID NOS: 79
:
: SEQ ID NO 75
:
: LENGTH: 245
:
: TYPE: PRT
:
: ORGANISM: artificial
:
US-08-918-148-75

```

Query Match	48.1%;	Score 785.5;	DB 4;	Length 245;
Best Local Similarity	64.0%;	Pred. NO. 2.8e-54;		
Matches 160; Conservative	29;	Mismatches 54;	Indels 7;	Gaps 4;

[illegible]

RESULT 15
US-08-918

```

US-08-918-148-76
? Sequence 76, Application US/08918148A
? Patent No. 6342220
? GENERAL INFORMATION:
? APPLICANT: Adams, Camellia
? APPLICANT: W.
? APPLICANT: Carter, Paul J.
? APPLICANT: Fendly, Brian M.
? APPLICANT: Gurney, Austin L.
? TITLE OF INVENTION: Agonist Antibody
? FILE REFERENCE: P0979
? CURRENT APPLICATION NUMBER: US/08/91
? CURRENT FILING DATE: 1997-08-25
? NUMBER OF SEQ ID NOS: 79
? SEQ ID NO 76
? LENGTH: 245
? TYPE: PRT
? ORGANSIM: arttificial
US-08-918-148-76

```

Query Match	48.0%;	Score 783.5;	DB 4;	Length 245;
Best Local Similarity	63.3%;	Pred. No. 4.1e-54;		
Matches 159;	Conservative 30;	Mismatches 53;	Indels 9;	Gaps 5;

QY	38	MAEVLQVQSGGVEPFGSLRLSCAASFTEDDYCMQSWQAPGKGLEVNSIINMGSGST	97
Db	1	MAEVLQVQSGGVEPFGSLRLSCAASFTEDDYCMQSWQAPGKGLEVNSIINMGSGST	60
QY	98	GYADSVKGRVITSRDANKNSLYLQNSLSRAEDTAVYYCAKILGAGRWY-FDLGKGTIV	156
Db	61	YVADSVKRFITSRNSKNTLYLQNSLSRAEDTAVYYCAR---DRSGTGMQVWGRTYV	116
QY	157	TVSSGGGSGGSGGSGGSS-ELFDDPA-VSVALGQVRFITCGGSLRSTVYASWYQOQKFG	214
Db	117	TVSSGGGSGGSGGSGGSGGSDIQMTDPSFTLSASIDRTYITTCRASEGITHLAWYQOQKFG	176
QY	215	QAPVLVIYIGKNNRPSGIPDRFSGSSSGNTASITITGAQDEADAYYCNSRDSGNNHYFG	274
Db	177	KAPKILLIYKASSLSAGPSRFSGSGGTDTLTISLPDPAFYTC-QQYSNYPPLTFG	234
QY	275	GGTKITVLGAA 265	
Db	235	GGTKLEITIRAA 245	

Search completed: September 22, 2003, 15:16:00
Job time : 19.2546 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 : Search time 51.7766 Seconds
(without alignments)
947.272 Million cell updates/sec

Title: US-10-052-798-9

Perfect score: 1633
Sequence: 1 MTMTTPSGAFLEIFNVKK.....HHGCAEDKILSEEDLNGAA 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_19Jun03:*

1: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1633	100.0	309	20	AAW83322
2	1633	100.0	309	23	ABW89603
3	1633	100.0	309	24	ABG74384
4	1460.5	89.4	312	20	AAW83323
5	1460.5	89.4	312	23	ABW89604
6	1460.5	89.4	312	24	ABG74385
7	1279.5	78.4	277	23	ABG92019
8	1279.5	78.4	277	23	ABG78328
9	1275.5	78.1	277	23	ABG91841

10	1275.5	78.1	277	23	ABG78150	Human Fv molecule
11	1231.5	75.4	310	20	AAW83324	Single chain Apo-2
12	1231.5	75.4	310	23	ABW89605	Amino acid sequenc
13	1231.5	75.4	310	24	ABG74386	Single chain antib
14	1223	74.9	266	23	ABG92020	Human antibody fra
15	1194.5	73.1	239	23	ABP46027	Human Blys binding
16	1189.5	72.8	239	23	ABP44926	Human Blys binding
17	1178.5	72.2	239	23	ABG46004	Human Blys binding
18	1178	72.1	246	23	ABG92026	Antibody protein #
19	1178	72.1	246	23	ABG78329	Human Fv molecule
20	1177	72.1	260	23	ABG92022	Antibody protein #
21	1171	71.7	256	23	ABG92025	Antibody biotag #1
22	1171	71.7	256	23	ABG78334	Human Fv molecule
23	1166.5	71.4	263	23	ABG92024	Antibody protein #
24	1155	70.7	282	23	AAE02185	PAM1 single chain
25	1139	69.7	240	23	ABP46002	Human Blys binding
26	1138	69.7	252	23	ABP45405	Human Blys binding
27	1133	69.4	238	21	AAV95198	Anti-platelet gIyc
28	1129	69.1	290	24	ABP55318	Human Blys binding
29	1122.5	68.7	239	23	ABG60637	Immunoglobulin rel
30	1122	68.7	296	23	ABG45312	Human Blys binding
31	1119	68.5	248	23	AAE29202	Single chain antib
32	1118.5	68.5	291	23	ABP46011	Human Blys binding
33	1116.5	68.4	239	23	ABG60632	Immunoglobulin rel
34	1116.5	68.4	291	23	ABG60632	Immunoglobulin rel
35	1116	68.3	248	23	ABP44905	Human Blys binding
36	1116	68.3	248	23	ABP44909	Human Blys binding
37	1113.5	68.2	239	23	ABP46007	Human Blys binding
38	1113.5	68.2	249	23	ABP45324	Human Blys binding
39	1112	68.1	248	23	ABP44824	Human Blys binding
40	1112	68.1	248	23	ABP44903	Human Blys binding
41	1111.5	68.1	241	23	ABP45900	Human Blys binding
42	1109.5	67.9	243	23	ABP46045	Human Blys binding
43	1109.5	67.9	249	23	ABP44952	Human Blys binding
44	1109.5	67.9	251	23	ABP45729	Human Blys binding
45	1108.5	67.9	239	23	ABP46024	Human Blys binding

ALIGNMENTS

RESULT 1
AAW83322
ID AAW83322 standard; Protein; 309 AA.
AC AAW83322;
DE 16-MAR-1999 (first entry)
XX Single chain Apo-2 antibody 16E2.
DE Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
KW TNF cytokine.
XX Homo sapiens.
OS WO9851793-A1.
XX 19-NOV-1998.
PD 14-MAY-1998; 98WO-US09704.
PE 09-FEB-1998; 98US-0020746.
PR 15-MAY-1997; 97US-0857216.
XX (GETH) GENENTECH INC.
PA Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
PI WPI: 1999-045228/04.
DR N-PSDB; AAV72532.
XX

PT Human Apo-2 polypeptide inducing apoptosis - useful to treat
PT conditions linked with decreased apoptosis e.g. cancer, and produce
PT antibodies to increase or decrease apoptosis

XX Example 14; Fig 16; 134pp; English.

CC The present invention describes human Apo-2. Apo-2 can be used
CC therapeutically to induce apoptosis in mammalian cells, and so is useful
CC to treat conditions associated with decreased apoptosis e.g. cancer.
CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor
CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by
CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It
CC can be used to identify agents activating Apo-2, useful to treat
CC mammalian cancer cells, and to produce Apo-2 chimeras useful
CC therapeutically (e.g. those containing immunoglobulin sequences can be
CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
CC tag polypeptide allow Apo-2 detection and purification using anti-tag
CC antibodies). It can be used to produce antibodies which can be combined
CC with a (particularly pharmacologically acceptable) carrier in compositions
CC or used to produce dimeric molecules (especially homodimeric molecules
CC comprising first and second Apo-2 antibodies). Agonistic (especially
CC single-chain) antibodies can be administered to induce apoptosis in
CC mammalian cancer cells, and antagonistic antibodies used to block
CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
CC antibodies may also be used diagnostically e.g. to detect Apo-2
CC expression in cells/tissues and in Apo-2 purification. The present
CC sequence represents a single chain Apo-2 antibody, designated 16E2.

XX Sequence 309 AA;

Query Match 100.0%; Score 1633; DB 20; Length 309;

Best Local Similarity 100.0%; Pred. No. 7.9e-101;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTMTSPFGAFLEIFNVKLLFAIPLVVFFYAAPAMAEVQLVOSGGVERPGSLRLS 60
DB 1 MTMTSPFGAFLEIFNVKLLFAIPLVVFFYAAPAMAEVQLVOSGGVERPGSLRLS 60
QY 61 CAASGTFDDYGSWVRQAPGKLEWVSGINMNGSGTGADSVKGRVTTISRDNAKNSLYL 120
DB 61 CAASGTFDDYGSWVRQAPGKLEWVSGINMNGSGTGADSVKGRVTTISRDNAKNSLYL 120
QY 121 QMNSLRADETAVYYCAKILGAGRGWYFDLMGKTTYVSSGGGSGGSGSSSELTQ 180
DB 121 QMNSLRADETAVYYCAKILGAGRGWYFDLMGKTTYVSSGGGSGGSGSSSELTQ 180
QY 181 DPAVSVALGQTVRITCGDSLRSYASWYQOKPGCAPLVYITGKNNRPGSIDPRFSGSSS 240
DB 181 DPAVSVALGQTVRITCGDSLRSYASWYQOKPGCAPLVYITGKNNRPGSIDPRFSGSSS 240
QY 241 GNTASLTITGAQAEDEADYYCNSRDSGSHNVYFGGSKTLVLGAANHHHHHGAADQKLI 300
DB 241 GNTASLTITGAQAEDEADYYCNSRDSGSHNVYFGGSKTLVLGAANHHHHHGAADQKLI 300
QY 301 SEEDLNGAA 309
DB 301 SEEDLNGAA 309
RESULT 2
ID ABB09603 standard; Protein; 309 AA.
XX ABB09603;
XX 29-MAY-2002 (first entry)
DE Amino acid sequence of single-chain Apo-2 antibody 16E2.
XX Human: Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;
XX caspase; apoptosis; cancer; antibody.
OS Bacteriophage.

XX US6342369-B1.
PN 29-JAN-2002.
XX

XX 14-MAY-1998; 98US-0079029.
XX

XX 15-MAY-1997; 97US-046615P.
XX 09-FEB-1998; 98US-074119P.
XX

PA (GETH) GENENTECH INC.

PI Ashkenazi AJ;

DR WPI: 2002-224941/28.

DR N-PDSB; ABEL41733.

PT New nucleic acids encoding an Apo-2 ligand, useful for activating or
PT stimulating apoptosis in cancer cells, thus especially useful in the
PT treatment of cancer, or in enhancing immune-mediated cell death

XX Example 14; Fig 16; 68pp; English.

CC The present sequence represents a single-chain Apo-2 antibody, designated
CC 16E2, which is isolated from a phage library. It is believed that
CC Apo-2 is a member of the tumour necrosis factor receptor (TNFR)
CC family. Apo-2 polypeptide is capable of triggering caspase-dependent
CC apoptosis and activating nuclear factor-kappa B. A soluble
CC extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2
CC antibodies may be used to activate or stimulate apoptosis in cancer
CC cells. They are therefore especially useful in the treatment of cancer,
CC to enhance immune-mediated cell death in cells expressing Apo-2, to
CC detect expression of Apo-2 in specific cells, tissues or serum, and in
CC affinity purification of Apo-2 from recombinant cell culture or natural
CC sources.

XX Sequence 309 AA;

Query Match 100.0%; Score 1633; DB 23; Length 309;

Best Local Similarity 100.0%; Pred. No. 7.9e-101;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTMTSPFGAFLEIFNVKLLFAIPLVVFFYAAPAMAEVQLVOSGGVERPGSLRLS 60
DB 1 MTMTSPFGAFLEIFNVKLLFAIPLVVFFYAAPAMAEVQLVOSGGVERPGSLRLS 60
QY 61 CAASGTFDDYGSWVRQAPGKLEWVSGINMNGSGTGADSVKGRVTTISRDNAKNSLYL 120
DB 61 CAASGTFDDYGSWVRQAPGKLEWVSGINMNGSGTGADSVKGRVTTISRDNAKNSLYL 120
QY 121 QMNSLRADETAVYYCAKILGAGRGWYFDLMGKTTYVSSGGGSGGSGSSSELTQ 180
DB 121 QMNSLRADETAVYYCAKILGAGRGWYFDLMGKTTYVSSGGGSGGSGSSSELTQ 180
QY 181 DPAVSVALGQTVRITCGDSLRSYASWYQOKPGCAPLVYITGKNNRPGSIDPRFSGSSS 240
DB 181 DPAVSVALGQTVRITCGDSLRSYASWYQOKPGCAPLVYITGKNNRPGSIDPRFSGSSS 240
QY 241 GNTASLTITGAQAEDEADYYCNSRDSGSHNVYFGGSKTLVLGAANHHHHHGAADQKLI 300
DB 241 GNTASLTITGAQAEDEADYYCNSRDSGSHNVYFGGSKTLVLGAANHHHHHGAADQKLI 300
QY 301 SEEDLNGAA 309
DB 301 SEEDLNGAA 309
RESULT 3
ID ABG74384 standard; Protein; 309 AA.
XX ABG74384;
XX ABG74384;
XX

DT 11-APR-2003 (first entry)
 XX Single chain antibody (scfv) fragment 16E2.
 DE
 XX
 KW Apo-2: tumour necrosis factor family; TNFR; gene therapy;
 KW apoptosis; tissue-specific typing; affinity purification;
 KW competitive-type receptor binding assay; mouse; 16E2.
 XX
 OS Mus sp.
 PN US2002150985-A1.
 PD 17-OCT-2002.
 XX
 PF 02-NOV-2001; 2001US-0052798.
 PR 15-MAY-1997; 97US-046615P.
 PR 09-FEB-1998; 98US-074119P.
 PR 14-MAY-1998; 98US-0079029.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
 DR WPI; 2003-198287/19.
 DR N-PSDB; ABX16407.
 XX
 PT New Apo-2 polypeptides and polynucleotides, useful for inducing
 PT apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in
 PT quantitative diagnostic assays, or in generating antibodies against
 PT Apo-2 -
 XX
 PS Example 14; Fig 16; 64pp; English.
 XX
 CC The invention describes a novel isolated Apo-2 polypeptide. The Apo-2
 CC polypeptide is useful for inducing apoptosis in mammalian cells, in vivo
 CC or ex vivo gene therapy, in quantitative diagnostic assays, as a control
 CC against samples containing unknown quantities of Apo-2, in generating
 CC antibodies, in affinity purification techniques, and in competitive-type
 CC receptor binding assays when labelled with, for instance, radiolodine,
 CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a
 CC diagnostic for tissue-specific typing. This is the amino acid sequence
 CC of the single chain antibody fragment (scfv) 16E2 used in the
 CC preparation of anti-apo-2 antibodies.
 CC
 CC Sequence 309 AA;
 SO
 Query Match 100.0%; Score 1633; DB 24; Length 309;
 Best Local Similarity 100.0%; Pred. No. 7.9e-101;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTMTSPRGAFLEIFNVKLLFAIPVPPYAOPMAEVLVOSGGVPRPGSLRLS 60
 DB 1 MTMTSPRGAFLEIFNVKLLFAIPVPPYAOPMAEVLVOSGGVPRPGSLRLS 60
 QY 61 CAASGTFEDDYGMKSVROAPGKLEWYSGIMNMGSGTADSVKGRYTIISDNKNSLYL 120
 DB 61 CAASGTFEDDYGMKSVROAPGKLEWYSGIMNMGSGTADSVKGRYTIISDNKNSLYL 120
 QY 121 QMNSLRBEDTAVYCAKILGAGRGWYFDLMGKGTTVVSSGGSGSGGSGSSSELTQ 180
 DB 121 QMNSLRBEDTAVYCAKILGAGRGWYFDLMGKGTTVVSSGGSGSGGSGSSSELTQ 180
 QY 121 QMNSLRBEDTAVYCAKILGAGRGWYFDLMGKGTTVVSSGGSGSGGSGSSSELTQ 180
 DB 121 QMNSLRBEDTAVYCAKILGAGRGWYFDLMGKGTTVVSSGGSGSGGSGSSSELTQ 180
 QY 181 DPAVASVALGOTVRITCGDLSRSYYASWYOOKPGOAPLVLYGKNNRPISGIPDFFSSSS 240
 DB 181 DPAVASVALGOTVRITCGDLSRSYYASWYOOKPGOAPLVLYGKNNRPISGIPDFFSSSS 240
 QY 241 GNTASLTITGAQADEADYCCNSRDSSGNHVFEGGTRKLTVLGAAGAHNNHNGAEOKLI 300
 DB 241 GNTASLTITGAQADEADYCCNSRDSSGNHVFEGGTRKLTVLGAAGAHNNHNGAEOKLI 300
 QY 301 SEEDLNGAA 309
 DB 301 SEEDLNGAA 309

DB 301 SEEDLNGAA 309
 RESULT 4
 ID AAW83323 standard; Protein: 312 AA.
 AC AAW83323;
 XX
 XX 16-MAR-1999 (first entry)
 DE Single chain Apo-2 antibody 20E6.
 XX
 XX Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
 KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
 KW TNF cytokine.
 XX
 OS Homo sapiens.
 PN M09851793-A1.
 PD 19-NOV-1998.
 XX
 PF 14-MAY-1998; 98WO-US09704.
 PR 09-FEB-1998; 98US-0020746.
 PR 15-MAY-1997; 97US-0857216.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
 DR WPI; 1999-045228/04.
 DR N-PSDB; AAV72533.
 XX
 PT Human Apo-2 polypeptide inducing apoptosis - useful to treat
 PT conditions linked with decreased apoptosis e.g. cancer, and produce
 PT antibodies to increase or decrease apoptosis
 XX
 PS Example 14; Fig 16; 134pp; English.
 XX
 CC The present invention describes human Apo-2. Apo-2 can be used
 CC therapeutically to induce apoptosis in mammalian cells, and so is useful
 CC to treat conditions associated with decreased apoptosis e.g. cancer.
 CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor
 CC (TNFR). TNF cytokines can induce apoptosis; thought to be initiated by
 CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It
 CC can be used to identify agents activating Apo-2, useful to treat
 CC mammalian cancer cells, and to produce Apo-2 chimeras useful
 CC therapeutically (e.g. those containing immunoglobulin sequences can be
 CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
 CC tag polypeptide allow Apo-2 detection and purification using anti-tag
 CC antibodies). It can be used to produce antibodies which can be combined
 CC with a (particularly pharmaceutically acceptable) carrier in compositions
 CC or used to produce dimeric molecules (especially homodimeric molecules
 CC comprising first and second Apo-2 antibodies). Agonistic (especially
 CC single-chain) antibodies can be administered to induce apoptosis in
 CC mammalian cancer cells, and antagonistic antibodies used to block
 CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
 CC antibodies may also be used diagnostically e.g. to detect Apo-2
 CC expression in cells/tissues and in Apo-2 purification. The present
 CC sequence represents a single chain Apo-2 antibody, designated 20E6.
 CC
 CC Sequence 312 AA;
 SO
 Query Match 89.4%; Score 1460.5; DB 20; Length 312;
 Best Local Similarity 90.1%; Pred. No. 2.2e-89;
 Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;
 QY 1 MTMTSPRGAFLEIFNVKLLFAIPVPPYAOPMAEVLVOSGGVPRPGSLRLS 60
 DB 1 MTMTSPRGAFLEIFNVKLLFAIPVPPYAOPMAEVLVOSGGVPRPGSLRLS 60

QY 61 CAASGFTDDYGMVSWROAPGKLEWVGIMNGSGTGYADSVKGRVTISRDNANKNSLYL 120
 ||||| 1 ||||| : : |||||
 Db 61 CAASGFTSSYWMVSWROAPGKLEWVANIKODGSEKYYVDSVKGRFTISRDNANKNSLYL 120
 QY 121 QMNSIRADDTAVYYCA---KILGARGMYFDLMKGTIVYSSGGSGSGSGSGSS 176
 ||||| : : |||||
 Db 121 QMNSIRADDTAVYYCARDLKVKGSSSGM-FDPWGRGTTIVYSSGGSGSGSGSGSS 179
 QY 177 ELTODPAVSVALGQTVRITTCOGDSLRSYYASWYQOKPGQAPLVLYGKNNRPSGIPDRFS 236
 ||||| : : |||||
 Db 180 ELTODPAVSVALGQTVRITTCOGDSLRSYYASWYQOKPGQAPLVLYGKNNRPSGIPDRFS 239
 QY 237 GSSSGNTASLTITGAQAEDEADYCNSSRDSSGNHVFSGGTRKLTVLGAHHHHHGAEE 296
 ||||| : : |||||
 Db 240 GSSSGNTASLTITGAQAEDEADYCNSSRDSSGNHVFSGGTRKLTVLGAHHHHHGAEE 299
 QY 297 QKLISEEDLNGAA 309
 |||||
 Db 300 QKLISEEDLNGAA 312

RESULT 5
 ABB09604
 ID ABB09604 standard; Protein; 312 AA.
 AC ABB09604;
 DT 29-MAY-2002 (first entry)

DE Amino acid sequence of single-chain Apo-2 antibody 20E6.

KM Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;
 KM caspase; apoptosis; cancer; antibody.
 OS Bacteriophage.

XX US642369-B1.
 PN 29-JAN-2002.
 PD 14-MAY-1998; 98US-0079029.
 PF 15-MAY-1997; 97US-046615P.
 PR 09-FEB-1998; 98US-074119P.
 XX (GETH) GENENTECH INC.

PA Ashkenazi AJ;

XX WPI: 2002-224941/28.
 DR N-PSDB; ABL41734.

PT New nucleic acids encoding an Apo-2 ligand, useful for activating or
 stimulating apoptosis in cancer cells; thus especially useful in the
 treatment of cancer, or in enhancing immune-mediated cell death
 Example 14; Fig 16; 68pp; English.

CC The present sequence represents a single-chain Apo-2 antibody, designated
 CC 20E6, which is isolated from a phage library. It is believed that
 CC Apo-2 is a member of the tumour necrosis factor receptor (TNFR)
 CC family. Apo-2 polypeptide is capable of triggering caspase-dependent
 CC apoptosis and activating nuclear factor-kappa B. A soluble
 CC extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2
 CC antibodies may be used to activate or stimulate apoptosis in cancer
 CC cells. They are therefore especially useful in the treatment of cancer,
 CC to enhance immune-mediated cell death in cells expressing Apo-2, to
 CC detect expression of Apo-2 in specific cells, tissues or serum, and in
 CC affinity purification of Apo-2 from recombinant cell culture or natural
 CC sources.

XX Sequence 312 AA;
 SQ

Query Match 89.4%; Score 1460.5; DB 23; Length 312;
 Best Local Similarity 90.1%; Pred. No. 2.2e-89;
 Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;

QY 1 MMTIPSPGAFLETFENYKILFALPLVPPFYAAQAPAAEYOLVOSGGVPPGSLRLS 60
 ||||| : : |||||
 Db 1 MMTIPSPGAFLETFENYKILFALPLVPPFYAAQAPAAEYOLVOSGGVPPGSLRLS 60
 QY 61 CAASGFTDDYGMVSWROAPGKLEWVGIMNGSGTGYADSVKGRVTISRDNANKNSLYL 120
 ||||| : : |||||
 Db 61 CAASGFTSSYWMVSWROAPGKLEWVANIKODGSEKYYVDSVKGRFTISRDNANKNSLYL 120
 QY 121 QMNSIRADDTAVYYCA---KILGARGMYFDLMKGTIVYSSGGSGSGSGSGSS 176
 ||||| : : |||||
 Db 121 QMNSIRADDTAVYYCARDLKVKGSSSGM-FDPWGRGTTIVYSSGGSGSGSGSGSS 179
 QY 177 ELTODPAVSVALGQTVRITTCOGDSLRSYYASWYQOKPGQAPLVLYGKNNRPSGIPDRFS 236
 ||||| : : |||||
 Db 180 ELTODPAVSVALGQTVRITTCOGDSLRSYYASWYQOKPGQAPLVLYGKNNRPSGIPDRFS 239
 QY 237 GSSSGNTASLTITGAQAEDEADYCNSSRDSSGNHVFSGGTRKLTVLGAHHHHHGAEE 296
 ||||| : : |||||
 Db 240 GSSSGNTASLTITGAQAEDEADYCNSSRDSSGNHVFSGGTRKLTVLGAHHHHHGAEE 299
 QY 297 QKLISEEDLNGAA 309
 |||||
 Db 300 QKLISEEDLNGAA 312

RESULT 6
 ABG74385
 ID ABG74385 standard; Protein; 312 AA.
 AC ABG74385;
 DT 11-APR-2003 (first entry)

DE Single chain antibody (scFv) fragment 20E6.

KM Apo-2; tumour necrosis factor family; TNFR; gene therapy;
 KM apoptosis; tissue-specific typing; affinity purification;
 KM competitive-type receptor binding assay; mouse; 20E6.

OS Mus sp.

XX US2002150985-A1.

PN 17-OCT-2002.

PD 02-NOV-2001; 2001US-0052798.

PF 15-MAY-1997; 97US-046615P.
 PR 09-FEB-1998; 98US-074119P.
 PR 14-MAY-1998; 98US-0079029.

XX (GETH) GENENTECH INC.

PA Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;

XX WPI: 2003-198287/19.
 DR N-PSDB; ABX16408.

PT New Apo-2 polypeptides and polynucleotides, useful for inducing
 PT apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in
 PT quantitative diagnostic assays, or in generating antibodies against
 Apo-2
 Example 14; Fig 16; 64pp; English.

CC The invention describes a novel isolated Apo-2 polypeptide. The Apo-2
 CC polypeptide is useful for inducing apoptosis in mammalian cells, in vivo
 CC or ex vivo gene therapy, in quantitative diagnostic assays, as a control
 CC against samples containing unknown quantities of Apo-2, in generating

CC antibodies, in affinity purification techniques, and in competitive-type
CC receptor binding assays when labelled with, for instance, radiiodine,
CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a
CC diagnostic for tissue-specific typing. This is the amino acid sequence
CC of the single chain antibody fragment (scFv) 20E6 used in the
CC preparation of anti-apo-2 antibodies.

XX Sequence 312 AA;

Query Match 89.4%; Score 1460.5; DB 24; Length 312;
Best Local Similarity 90.1%; Pred. No. 2.2e-89;
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;

QY 1 MTMTSPFGAFLEIFNVKLLFAIPLVPEYAAQPMAMAEVOLVQSGGVERPGSLRLS 60
DB 1 MTMTSPFGAFLEIFNVKLLFAIPLVPEYAAQPMAMAEVOLVQSGGVERPGSLRLS 60
QY 61 CAAGGTFPDYGMWVQAPKGLKLEWVSGIMNGSGTGADSVKGRVTISDNKNSLYL 120
DB 61 CAAGGTFPDYGMWVQAPKGLKLEWVSGIMNGSGTGADSVKGRVTISDNKNSLYL 120
QY 121 QMNSLRADPFAVYCA---KILGAGRWYFDLWKGTVTVSSGGSGSGSGSGSS 176
DB 121 QMNSLRADPFAVYCA---KILGAGRWYFDLWKGTVTVSSGGSGSGSGSGSS 176
QY 121 QMNSLRADPFAVYCA---KILGAGRWYFDLWKGTVTVSSGGSGSGSGSGSS 179
DB 121 QMNSLRADPFAVYCA---KILGAGRWYFDLWKGTVTVSSGGSGSGSGSGSS 179
QY 177 ELTQDPFAVVALGQTVRITCGDSLRSYASWYQKPGQAPVLVLYGKNNRPGSIPRFS 236
DB 177 ELTQDPFAVVALGQTVRITCGDSLRSYASWYQKPGQAPVLVLYGKNNRPGSIPRFS 236
QY 180 ELTQDPFAVVALGQTVRITCGDSLRSYASWYQKPGQAPVLVLYGKNNRPGSIPRFS 239
DB 180 ELTQDPFAVVALGQTVRITCGDSLRSYASWYQKPGQAPVLVLYGKNNRPGSIPRFS 239
QY 237 GSSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTFLVLAANHHNHGAAE 296
DB 237 GSSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTFLVLAANHHNHGAAE 296
QY 240 GSSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTFLVLAANHHNHGAAE 299
DB 240 GSSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTFLVLAANHHNHGAAE 299
QY 297 OKLISEEDLNGAA 309
DB 297 OKLISEEDLNGAA 312

RESULT 7
ABG92019 ID ABG92019 standard; Protein: 277 AA.

XX ABG92019;
XX 04-DEC-2002 (first entry)

DE Human antibody fragment #203.

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW reticentosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.

XX Homo sapiens.

XX MO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001WO-US49442.

XX 29-DEC-2000; 2000US-258948P.

XX 29-DEC-2000; 2000US-0751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Lazarevits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;

XX Szeanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in

PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer

PS Claim 23; Page 308-309; 310pp; English.

XX The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, reticentosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,
CC platelet-platelet and/or cell-platelet adhesion or aggregation, for
CC increasing mortality of tumour or leukaemia cells, for increasing the
CC susceptibility of diseased cells to damage by anti-disease, anti-cancer
CC or anti-leukaemia agents, or for decreasing the number of tumour or
CC leukaemia cells in a patient, or in the manufacture of a medicament for
CC the above mentioned purposes. The epitopes are useful for diagnosing and
CC treating diseases such as cancer, leukaemia, autoimmune diseases,
CC inflammatory diseases, cardiovascular diseases such as myocardial
CC infarction, retinopathic diseases and other diseases mediated by abnormal
CC platelet function and diseases caused by sulphated tyrosine-dependent
CC protein-protein interactions. This sequence represents a human antibody
CC fragment of the invention.

SO Sequence 277 AA;

Query Match 78.4%; Score 1279.5; DB 23; Length 277;
Best Local Similarity 90.6%; Pred. No. 2e-77;
Matches 251; Conservative 4; Mismatches 7; Indels 15; Gaps 3;

QY 33 AADPAMAEVOLVQSGGVERPGSLRLSCAAGTFPDYGMWVQAPKGLKLEWVSGINW 92
DB 16 AADPAMAEVOLVQSGGVERPGSLRLSCAAGTFPDYGMWVQAPKGLKLEWVSGINW 92
QY 93 NGSGTGYADSVKGRVTISRDNAKNSLYLQMSLRAEDPAVYCAKILGAGWTFDLMGK 152
DB 76 NGSGTGYADSVKGRVTISRDNAKNSLYLQMSLRAEDPAVYCAKILGAGWTFDLMGK 152
QY 153 GTTVTVSSGGSGSGSGSGSGSELTDPAVVALGQTVRITCGDSLRSYASWYQK 212
DB 130 GTTVTVSSGGSGSGSGSGSGSELTDPAVVALGQTVRITCGDSLRSYASWYQK 212
QY 213 PGQAPVLVLYGKNNRPGSIPRFSGSSGNTASLTITTAQAEDEADYYCNSRDSGNNHV 272
DB 190 PGQAPVLVLYGKNNRPGSIPRFSGSSGNTASLTITTAQAEDEADYYCNSRDSGNNHV 249
QY 273 FGGGKTFLVLAANHHNHGAAEOKLISEEDLNGAA 309
DB 250 FGGGKTFLVLAANHHNHGAAEOKLISEEDLNGAA 277

RESULT 8
ABG78328 ID ABG78328 standard; Protein: 277 AA.

XX ABG78328;

XX 15-NOV-2002 (first entry)

XX Human Fv molecule hypervariable region related peptide #203.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW disulfide Fv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX Homo sapiens.

XX MO200259264-A2.

XX

PD 01-AUG-2002.
XX
XX 31-DEC-2001; 2001WO-US49440.
XX
XX 29-DEC-2000; 2000US-0751181.
XX
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
PI Plaksin D, Peretz T;
XX
XX WPI: 2002-619166/66.
DR N-PSDB; ABS63384.
XX
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favour of other
PT cells -
XX
XX Claim 141; Fig 14; 232pp; English.
XX
XX The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the Leukaemia cell is an
CC acute myeloid Leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention.
XX
XX Sequence 277 AA:
SQ
Query Match 78.4%; Score 1279.5; DB 23; Length 277;
Best Local Similarity 90.6%; Pred. No. 2e-77;
Matches 251; Conservative 4; Mismatches 7; Indels 15; Gaps 3;
QY 33 AAQPMAAEVQLVQSGGVEVERPGSRLSCAASGFTFPDDYGMWVRQAPGKGLEWVSGINW 92
DB 16 AAQPMAAEVQLVESGGGVVRRPGSRLSCAASGFTFPDDYGMWVRQAPGKGLEWVSGINW 75
QY 93 NGSTGYADSVKGRVLTISRDNAKNSLYLQMNSLRADPVAVYCAKILGARGWYFDLMGK 152
DB 76 NGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRADPVAVYCAKILGHP----YF--WGQ 129
QY 153 GTTVTVSSGGSGGGSGGSSSELTQDPAVSVALGQTVRITCGDSLRSYASYWYQOK 212
DB 130 GTLVTVSRGGSGGGSGGSSSELTQDPAVSVALGQVTRITCGDSLRSYASYWYQOK 189
QY 213 PGQAPVLYLYGKNNRPSGIPDRFSSSSSNTASTLTITGAQADEADYCNSSDSSGNHYV 272
DB 190 PGQAPVLYLYGKNNRPSGIPDRFSSSSSNTASTLTITGAQADEADYCNSSDSSGNHYV 249
QY 273 FCGGTRLTVLGAAGHHHGAEOKLISEEDLNGAA 309
DB 250 FCGGTRLTVLGA-----AABOKLISEEDLNGAA 277
RESULT 9
ABG91841
ID ABG91841 standard; Protein; 277 AA.
XX
XX ABG91841;
AC
XX 04-DEC-2002 (first entry)
DT
XX
XX Human antibody fragment #25.

XX
XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
XX Homo sapiens.
OS
XX
XX WO200253700-A2.
PN
XX
XX 11-JUL-2002.
PD
XX
XX 31-DEC-2001; 2001WO-US49442.
PF
XX
XX 29-DEC-2000; 2000US-258948P.
PR
XX 29-DEC-2000; 2000US-0751181.
XX
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
XX WPI: 2002-674776/72.
DR
XX
XX Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer -
XX
XX Claim 23; Page 233-234; 310pp; English.
XX
XX The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,
CC platelet-platelet and/or cell-platelet adhesion or aggregation, for
CC increasing mortality of tumour or leukaemia cells, for increasing the
CC susceptibility of diseased cells to damage by anti-disease, anti-cancer
CC or anti-leukaemia agents, or for decreasing the number of tumour or
CC leukaemia cells in a patient, or in the manufacture of a medicament for
CC the above mentioned purposes. The epitopes are useful for diagnosing and
CC treating diseases such as cancer, leukemia, autoimmune diseases,
CC inflammatory diseases, cardiovascular diseases such as myocardial
CC infarction, retinopathic diseases and other diseases mediated by abnormal
CC platelet function and diseases caused by sulphated tyrosine-dependent
CC protein-protein interactions. This sequence represents a human antibody
CC fragment of the invention.
XX
XX Sequence 277 AA:
SQ
Query Match 78.1%; Score 1275.5; DB 23; Length 277;
Best Local Similarity 89.9%; Pred. No. 3.7e-77;
Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;
QY 33 AAQPMAAEVQLVQSGGVEVERPGSRLSCAASGFTFPDDYGMWVRQAPGKGLEWVSGINW 92
DB 16 AAQPMAAEVQLVESGGGVVRRPGSRLSCAASGFTFPDDYGMWVRQAPGKGLEWVSGINW 75
QY 93 NGSTGYADSVKGRVLTISRDNAKNSLYLQMNSLRADPVAVYCAKILGARGWYFDLMGK 152
DB 76 NGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRADPVAVYCAKILGARGWYFDLMGK 129
QY 153 GTTVTVSSGGSGGGSGGSSSELTQDPAVSVALGQTVRITCGDSLRSYASYWYQOK 212
DB 130 GTLVTVSRGGSGGGSGGSSSELTQDPAVSVALGQVTRITCGDSLRSYASYWYQOK 189
QY 213 PGQAPVLYLYGKNNRPSGIPDRFSSSSSNTASTLTITGAQADEADYCNSSDSSGNHYV 272

Db 190 PGOAPVLYIYKNNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSSGNHV 249
 QY 273 FGGGTKLTVLGAHHHHHGAEOKLISEEDLNGAA 309
 Db 250 FGGGTKLTVLGA-----AAEOKLISEEDLNGAA 277

RESULT 10
 ABG78150
 ID ABG78150 standard; Protein: 277 AA.
 AC ABG78150;
 DT 15-NOV-2002 (first entry)
 DE Human Fv molecule hypervariable region related peptide #25.
 XX
 KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX Homo sapiens.
 OS WO200259264-A2.
 PN 01-AUG-2002.
 PD 31-DEC-2001; 2001WO-US49440.
 PF 29-DEC-2000; 2000US-0751181.
 PR (BIOT-) BIO-TECHNOLOGY GEN CORP.
 PA Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A; Plakstin D, Peretz T;
 PI WPI; 2002-619166/66.
 DR
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favour of other cells -
 PT
 PS Claim 4; Page 155-156; 232pp; English.
 CC The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region related peptide of the invention.
 CC
 XX Sequence 277 AA;
 SO

Query Match 78.1%; Score 1275.5; DB 23; Length 277;
 Best Local Similarity 89.9%; Pred. No. 3.7e-77;
 Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;

QY 33 AAOAPMAEVOLYOGSGGVERGSLRISCAASGTFPDYGSWVRQAGKLEWVSGINW 92
 Db 16 AAOAPMAEVOLYOGSGGVERGSLRISCAASGTFPDYGSWVRQAGKLEWVSGINW 75
 QY 93 NGSGTYADSVKGVHTTISRDNKNSLYLQNNSLRAEDTAVYVYCAKILGAGRGWFDLWGK 152

Db 76 NGSGTYADSVKGVHTTISRDNKNSLYLQNNSLRAEDTAVYVYCAKILGAGRGWFDLWGK 129
 QY 153 GTTYVSSGGGGGGGGGGSSSLTDDPAVSAVLSGTVYRTCGDLSRYSYASWYQK 212
 Db 130 GTLYVSSKGGGSGGGGGSSSLTDDPAVSAVLSGTVYRTCGDLSRYSYASWYQK 189
 QY 213 PGOAPVLYIYKNNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSSGNHV 272
 Db 190 PGOAPVLYIYKNNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSSGNHV 249
 QY 273 FGGGTKLTVLGAHHHHHGAEOKLISEEDLNGAA 309
 Db 250 FGGGTKLTVLGA-----AAEOKLISEEDLNGAA 277

RESULT 11
 AAW83324
 ID AAW83324 standard; Protein: 310 AA.
 AC AAW83324;
 DT 16-MAR-1999 (first entry)
 DE Single chain Apo-2 antibody 24C4.
 XX
 KW Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer; tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR; TNF cytokine.
 XX Homo sapiens.
 OS WO9851793-A1.
 PN 19-NOV-1998.
 PD 14-MAY-1998; 98WO-US09704.
 PF 09-FEB-1998; 98US-0020746.
 PR 15-MAY-1997; 97US-0857216.
 PA (GETH) GENENTECH INC.
 PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
 DR WPI; 1999-045228/04.
 DR N-PSDB; AAV72534.
 XX Human Apo-2 polypeptide inducing apoptosis - useful to treat conditions linked with decreased apoptosis e.g. cancer, and produce antibodies to increase or decrease apoptosis
 PT
 PS Example 14; Fig 16; 134pp; English.
 CC The present invention describes human Apo-2. Apo-2 can be used therapeutically to induce apoptosis in mammalian cells, and so is useful to treat conditions associated with decreased apoptosis e.g. cancer. Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It can be used to identify agents activating Apo-2, useful to treat mammalian cancer cells, and to produce Apo-2 chimeras useful therapeutically (e.g. those containing immunoglobulin sequences can be inhibit apoptosis) or diagnostically (e.g. those comprising an epitope tag polypeptide allow Apo-2 detection and purification using anti-tag antibodies). It can be used to produce antibodies which can be combined with a (particularly pharmaceutically acceptable) carrier in compositions or used to produce dimeric molecules (especially homodimeric molecules comprising first and second Apo-2 antibodies). Agonistic (especially single-chain) antibodies can be administered to induce apoptosis in mammalian cancer cells, and antagonistic antibodies used to block excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2 antibodies may also be used diagnostically e.g. to detect Apo-2

CC expression in cells/tissues and in Apo-2 purification. The present
 CC sequence represents a single chain Apo-2 antibody, designated 24C4.

SQ Sequence 310 AA;

Query Match 75.4%; Score 1231.5; DB 20; Length 310;
 Best Local Similarity 78.0%; Pred. No. 3.5e-74;
 Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

QY 1 MTMTSPGAFPLEIFNNVKKLLFAIPLVYFPAAPAMAEVOLVDSGGGVERRPGSLRLS 60
 DB 1 MTMTSPGAFPLEIFNNVKKLLFAIPLVYFPAAPAMAEVOLVDSGGGVERRPGSLRLS 60
 QY 61 CAASGTFDDYGMASVWRQAPGKGLVWVSGINNNGSGTGADSVKGRVITSRDANKSLYL 120
 DB 61 CAASGFIFSSYGMHWRQAPGKGLVWVAGIFYDGNKRYADSVKGRFTISRDNKNTLYL 120
 QY 121 QNNSLRAEPTAVYCAKILGAGRWTF--DLMGKFTTVYVSSGGSGSGGSGGSQSVL 178
 DB 121 QNNSLRAEPTAVYCAR---DRGYTMDVMGKGTTVYVSSGGSGSGGSGGSQSVL 176
 QY 179 TDDPAVSVALGQTVRITTCGDSLRL--SYAASWYQKPGQAPVLVYIGKNNRPSGIPDRF 235
 DB 177 TQPPSVSAGAPGQRTVITCTGRSSNIGAGHDVHMVQQLPETAARKLLYDSDNRPSPVDRF 236
 QY 236 SCSSSGNTASLTITGAQAEDEADYYCNSRDSGNHNVFEGGTRKLVYGAANHHNHGAA 295
 DB 237 SGRSGTSAISLAITGLQAEDEADYYCQSYDSLRSGSVFGGTRKLVYGAANHHNHGAA 296
 QY 296 EOKLISEDLNGAA 309
 DB 297 EOKLISEDLNGAA 310

RESULT 12

AB09605 ID ABB09605 standard; Protein; 310 AA.

XX ABB09605;

DT 29-MAY-2002 (first entry)

XX Amino acid sequence of single-chain Apo-2 antibody 24C4.

XX Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;
 KW caspase; apoptosis; cancer; antibody.

OS Bacteriophage.

PN US6342369-B1.

PD 29-JAN-2002.

PF 14-MAY-1998; 98US-0079029.

PR 15-MAY-1997; 97US-046615P.

PR 09-FEB-1998; 98US-074119P.

PA (GETH) GENENTECH INC.

PI Ashkenazi AJ;

DR WPI; 2002-224941/28.

DR N-PSDB; ABL41735.

PT New nucleic acids encoding an Apo-2 ligand, useful for activating or
 PT stimulating apoptosis in cancer cells; thus especially useful in the
 PT treatment of cancer, or in enhancing immune-mediated cell death

XX Example 14; Fig 16; 68pp; English.

CC The present sequence represents a single-chain Apo-2 antibody, designated
 CC 24C4, which is isolated from a phage library. It is believed that

CC Apo-2 is a member of the tumour necrosis factor receptor (TNFR)
 CC family. Apo-2 polypeptide is capable of triggering caspase-dependent
 CC apoptosis and activating nuclear factor-kappa B. A soluble
 CC extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2
 CC antibodies may be used to activate or stimulate apoptosis in cancer
 CC cells. They are therefore especially useful in the treatment of cancer,
 CC to enhance immune-mediated cell death in cells expressing Apo-2, to
 CC detect expression of Apo-2 in specific cells, tissues or serum, and in
 CC affinity purification of Apo-2 from recombinant cell culture or natural
 CC sources.

SQ Sequence 310 AA;

Query Match 75.4%; Score 1231.5; DB 23; Length 310;
 Best Local Similarity 78.0%; Pred. No. 3.5e-74;
 Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

QY 1 MTMTSPGAFPLEIFNNVKKLLFAIPLVYFPAAPAMAEVOLVDSGGGVERRPGSLRLS 60
 DB 1 MTMTSPGAFPLEIFNNVKKLLFAIPLVYFPAAPAMAEVOLVDSGGGVERRPGSLRLS 60
 QY 61 CAASGTFDDYGMASVWRQAPGKGLVWVSGINNNGSGTGADSVKGRVITSRDANKSLYL 120
 DB 61 CAASGFIFSSYGMHWRQAPGKGLVWVAGIFYDGNKRYADSVKGRFTISRDNKNTLYL 120
 QY 121 QNNSLRAEPTAVYCAKILGAGRWTF--DLMGKFTTVYVSSGGSGSGGSGGSQSVL 178
 DB 121 QNNSLRAEPTAVYCAR---DRGYTMDVMGKGTTVYVSSGGSGSGGSGGSQSVL 176
 QY 179 TDDPAVSVALGQTVRITTCGDSLRL--SYAASWYQKPGQAPVLVYIGKNNRPSGIPDRF 235
 DB 177 TQPPSVSAGAPGQRTVITCTGRSSNIGAGHDVHMVQQLPETAARKLLYDSDNRPSPVDRF 236
 QY 236 SCSSSGNTASLTITGAQAEDEADYYCNSRDSGNHNVFEGGTRKLVYGAANHHNHGAA 295
 DB 237 SGRSGTSAISLAITGLQAEDEADYYCQSYDSLRSGSVFGGTRKLVYGAANHHNHGAA 296
 QY 296 EOKLISEDLNGAA 309
 DB 297 EOKLISEDLNGAA 310

RESULT 13

ABG74386 ID ABG74386 standard; Protein; 310 AA.

XX ABG74386;

DT 11-APR-2003 (first entry)

DE Single chain antibody (scFv) fragment 24C4.

XX Apo-2; tumour necrosis factor family; TNFR; gene therapy;
 KW apoptosis; tissue-specific typing; affinity purification;
 KW competitive-type receptor binding assay; mouse; 24C4.

OS Mus sp.

PN US2002150985-A1.

PD 17-OCT-2002.

PF 02-NOV-2001; 2001US-0052798.

PR 15-MAY-1997; 97US-046615P.

PR 09-FEB-1998; 98US-074119P.

PR 14-MAY-1998; 98US-0079029.

PA (GETH) GENENTECH INC.

PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;

DR WPI; 2003-198287/19.

DR N-PSDB; ABX16409.
XX
PT New Apo-2 polypeptides and polynucleotides, useful for inducing
PT apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in
PT quantitative diagnostic assays, or in generating antibodies against
PT Apo-2.
XX
PS Example 14; Fig 16; 64pp; English.
XX
CC The invention describes a novel isolated Apo-2 polypeptide. The Apo-2
CC polypeptide is useful for inducing apoptosis in mammalian cells, in vivo
CC or ex vivo gene therapy, in quantitative diagnostic assays, as a control
CC against samples containing unknown quantities of Apo-2, in generating
CC antibodies, in affinity purification techniques, and in competitive-type
CC receptor binding assays when labelled with, for instance, radioiodine,
CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a
CC diagnostic for tissue-specific typing. This is the amino acid sequence
CC of the single chain antibody fragment (scFv) 24C4 used in the
CC preparation of anti-apo-2 antibodies.
XX
SQ Sequence 310 AA:
Query Match 75.4%; Score 1231.5; DB 24; Length 310;
Best Local Similarity 78.0%; Pred. No. 3.5e-74;
Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;
QY 1 MFMTPSEGAFFLEIFNVKLLFAIPVPEYAAQPMAMVQVQSGGVERPGSRLS 60
DB 1 MFMTPSEGAFFLEIFNVKLLFAIPVPEYAAQPMAMVQVQSGGVERPGSRLS 60
QY 61 CAASGFTFDYDGMVSWQARFGKLEWVSGINMGSGTGYADSVKGYTISRDNKNSLYL 120
DB 61 CAASGFTFDYDGMVSWQARFGKLEWVSGINMGSGTGYADSVKGYTISRDNKNSLYL 120
QY 121 QMNSLRADTAVYCAKILGAGKGYR-DLMGKTYTVSSGGGSGGSGGSGGSG-SEL 178
DB 121 QMNSLRADTAVYCAKILGAGKGYR-DLMGKTYTVSSGGGSGGSGGSGGSGGSG-SEL 178
QY 179 TQDPAVVALGQVYRIRTCGGDSLK---SYASWYQKPGQAPVLYITGKNNRPGGIDRF 235
DB 179 TQDPAVVALGQVYRIRTCGGDSLK---SYASWYQKPGQAPVLYITGKNNRPGGIDRF 235
QY 177 TQPPSVGAPQQRITICTGRSSNIGAGHDVHMVQQLPGRAPKLLITDDSNRPGVDRF 236
DB 177 TQPPSVGAPQQRITICTGRSSNIGAGHDVHMVQQLPGRAPKLLITDDSNRPGVDRF 236
QY 236 SGSSSGNTASLTITGAQDEADYVYCNRSRDSGNHVVFGGKTLTVLGAAAHNNHNGAA 295
DB 236 SGSSSGNTASLTITGAQDEADYVYCNRSRDSGNHVVFGGKTLTVLGAAAHNNHNGAA 295
QY 296 EOKLISEEDLNGAA 309
DB 296 EOKLISEEDLNGAA 310
RESULT 14
ABG92020
ID ABG92020 standard; Protein: 266 AA.
XX
AC ABG92020;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human antibody fragment #204.
XX
KW Human: antibody; epitope: cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX

PF 31-DEC-2001; 2001WO-US49442.
XX
XX 29-DEC-2000; 2000US-258948P.
PR 29-DEC-2000; 2000US-0751181.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Stanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX WPI: 2002-674776/72.
DR
XX
XX Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX
PS Disclosure: Page 309-310; 310pp; English.
XX
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,
CC platelet-platelet and/or cell-platelet adhesion or aggregation, for
CC increasing mortality of tumour or leukaemia cells, for increasing the
CC susceptibility of diseased cells to damage by anti-disease, anti-cancer
CC or anti-leukaemia agents, or for decreasing the number of tumour or
CC leukaemia cells in a patient, or in the manufacture of a medicament for
CC the above mentioned purposes. The epitopes are useful for diagnosing and
CC treating diseases such as cancer, leukaemia, autoimmune diseases,
CC inflammatory diseases, cardiovascular diseases such as myocardial
CC infarction, retinopathic diseases and other diseases mediated by abnormal
CC platelet function and diseases caused by sulphated tyrosine-dependent
CC protein-protein interactions. This sequence represents a human antibody
CC fragment of the invention.
XX
SQ Sequence 266 AA:
Query Match 74.9%; Score 1223; DB 23; Length 266;
Best Local Similarity 92.5%; Pred. No. 1.1e-73;
Matches 235; Conservative 5; Mismatches 8; Indels 6; Gaps 1;
QY 33 AAQPMAMEVQVQSGGVERPGSLRLSCAASGFTFDYDGMVSWQARFGKLEWVSGINW 92
DB 16 AAQPMAMEVQVQSGGVERPGSLRLSCAASGFTFDYDGMVSWQARFGKLEWVSGINW 75
QY 93 NGSGTYADSVKGYTISRDNKNSLYLQMSLRADTAVYCAKILGAGKGYTDLWGK 152
DB 76 NGSGTYADSVKGYTISRDNKNSLYLQMSLRADTAVYCAKILGAGKGYTDLWGK 129
QY 153 GTTPTVSSGGGSGGSGGSGGSGGSELTQDPAVVALGQVYRIRTCGGDSLTVASWYQK 212
DB 130 GTTPTVSSGGGSGGSGGSGGSGGSELTQDPAVVALGQVYRIRTCGGDSLTVASWYQK 189
QY 213 PGQAPVLYITGKNNRPGGIDRFSGSSSGNTASLTITGAQDEADYVYCNRSRDSGNHVV 272
DB 190 PGQAPVLYITGKNNRPGGIDRFSGSSSGNTASLTITGAQDEADYVYCNRSRDSGNHVV 249
QY 273 FGGGKTITVGGAA 286
DB 250 FGGGKTITVGGAA 263
RESULT 15
ABP46027
ID ABP46027 standard; Protein: 239 AA.
XX
AC ABP46027;
XX

XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 2038.
DE
XX
KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US19110.
XX
XX 16-JUN-2000; 2000US-212210P.
XX 17-OCT-2000; 2000US-240816P.
XX 16-MAR-2001; 2001US-276248P.
XX 21-MAR-2001; 2001US-277379P.
XX 25-MAY-2001; 2001US-293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B lymphocyte stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
XX Claim 1: Page 2830-2831; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX
SQ Sequence 239 AA;

Query Match 73.1%; Score 1194.5; DB 23; Length 239;
Best Local Similarity 93.4%; Pred. No. 7.6e-72;
Matches 228; Conservative 4; Mismatches 7; Indels 5; Gaps 1;
QY 40 EVOLVQSGGGERPGSGLRLSCAASGTFEDDYGMSVVRQAPGKLEWYSGINMNGSGTGY 99
DB 1 EVQLVESGGGVYVRPGSGLRSLCAASGTFEDDYGMSVVRQAPGKLEWYSGINMNGSGTGY 60
QY 100 ADSVGRYTIISDNKNSLYLQMSLRAPDTAVYYCAKTLGAGRGYEDLWKGKTTVYS 159
DB 61 ADSVGRFTISRDNKNSLYLQMSLRAPDTAVYYCAR-----RRYALDYWGQGLTVYS 115
QY 160 SGGGSGGGSGGGSGGSELTQDPAVSVALGQTVRITCGDSLRSYYASWYQKPGQAPVL 219
DB 116 SGGGSGGGSGGGSGGSELTQDPAVSVALGQTVRITCGDSLRSYYASWYQKPGQAPVL 175

QY 220 VIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYICNSRDSGNNHVFGGGTRL 279
DB 176 VIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYICNSRDSGNNHVFGGGTRL 235
QY 280 TVLG 283
DB 236 TVLG 239

Search completed: September 22, 2003, 15:18:43
Job time : 52.7766 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:16:07 : Search time 34.1858 Seconds
(without alignments)
1345.823 Million cell updates/sec

Title: US-10-052-798-9

Perfect score: 1633
Sequence: 1 MTMTSPGAFLEIFNVKK.....HHHCAPQKLISEEDLNGAA 309

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 556269 seqs, 148893369 residues

Total number of hits satisfying chosen parameters: 556269

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCRUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1633	100.0	309	12	US-10-288-917-9
2	1633	100.0	309	12	US-10-052-798-9
3	1460.5	89.4	312	14	US-10-288-917-10
4	1460.5	89.4	312	14	US-10-052-798-10
5	1231.5	75.4	310	12	US-10-288-917-11
6	1231.5	75.4	310	14	US-10-052-798-11
7	1194.5	73.1	239	11	US-09-880-748-2038
8	1189.5	72.8	239	11	US-09-880-748-937
9	1178.5	69.7	239	11	US-09-880-748-2015
10	1139	69.7	240	11	US-09-880-748-2013
11	1138	69.7	252	11	US-09-880-748-1416
12	1129	69.1	290	12	US-09-969-748C-2
13	1129	69.1	290	12	US-09-949-039-2
14	1122.5	68.7	239	11	US-09-880-748-2023
15	1122	68.7	296	12	US-09-969-748C-12

16 1122 68.7 296 12 US-09-949-039-75
17 1119 68.5 248 11 US-09-880-748-1323
18 1116.5 68.4 239 11 US-09-880-748-2022
19 1116 68.3 248 11 US-09-880-748-916
20 1116 68.3 248 11 US-09-880-748-920
21 1113.5 68.2 239 11 US-09-880-748-2018
22 1113.5 68.2 249 11 US-09-880-748-1335
23 1112 68.1 248 11 US-09-880-748-835
24 1112 68.1 248 11 US-09-880-748-911
25 1111.5 68.1 241 11 US-09-880-748-2036
26 1109.5 67.9 243 11 US-09-880-748-2056
27 1109.5 67.9 249 11 US-09-880-748-963
28 1109.5 67.9 251 11 US-09-880-748-1740
29 1108.5 67.9 239 11 US-09-880-748-2035
30 1108.5 67.9 251 11 US-09-880-748-952
31 1105.5 67.7 243 11 US-09-880-748-1929
32 1102.5 67.5 247 11 US-09-880-748-996
33 1102.5 67.5 249 11 US-09-880-748-1109
34 1101.5 67.5 245 11 US-09-880-748-1826
35 1101.5 67.5 247 11 US-09-880-748-1764
36 1101.5 67.5 251 11 US-09-880-748-908
37 1101.5 67.5 251 11 US-09-880-748-982
38 1101 67.4 246 11 US-09-880-748-1975
39 1099.5 67.3 247 11 US-09-880-748-1703
40 1098.5 67.3 243 11 US-09-880-748-1942
41 1098.5 67.3 247 11 US-09-880-748-924
42 1098 67.2 248 11 US-09-880-748-913
43 1097.5 67.2 237 11 US-09-880-748-2039
44 1097.5 67.2 237 11 US-09-880-748-2112
45 1096.5 67.1 243 11 US-09-880-748-1940

ALIGNMENTS

RESULT 1
US-10-288-917-9
: Sequence 9, Application US/10288917
: Publication No. US20030148455A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
Ashkenazi, Avi J.
Chuntharapai, Anan
Kim, Kyung J.

TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco
STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/288,917

FILING DATE: 06-NO. US20030148455A1-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 10/052798

FILING DATE: 02-NOV-2001

APPLICATION NUMBER: 09/079029

FILING DATE: 14-MAY-1998

APPLICATION NUMBER: 60/074119

FILING DATE: 09-FEB-1998

APPLICATION NUMBER: 60/046615

FILING DATE: 15-MAY-1997

ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.


```

? REGISTRATION NUMBER: 35,600
? REFERENCE/DOCKET NUMBER: P1101
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650/225-5416
? TELEFAX: 650/952-9881
? INFORMATION FOR SEQ ID NO: 9:
?     SEQUENCE CHARACTERISTICS:
?     LENGTH: 309 amino acids
?     TYPE: Amino Acid
?     TOPOLOGY: linear
?     SEQUENCE DESCRIPTION: SEQ ID NO: 9
US-10-288-917-9

```

Query Match	100.0%	Score 1633;	DB 12	Length 309;
Best Local Similarity	100.0%	Pred. No. 8, 5e-108;		
Matches 309; Conservative	0;	Mismatches	0;	Indels 0
				Gaps 0

QY	1	MTMTIPSPGAEFLTEFNKKLLFALPLVYFPAAGRAMAEVOLVSGGGERGGSLRLS	60
Db	1	MTMTIPSPGAEFLTEFNKKLLFALPLVYFPAAGRAMAEVOLVSGGGERGGSLRLS	60
QY	61	CAASGFTDDYDGMVNRQAPGKGLEWSSINNGSGTGADSYKGRVTTISRDNAKNSLYL	120
Db	61	CAASGFTDDYDGMVNRQAPGKGLEWSSINNGSGTGADSYKGRVTTISRDNAKNSLYL	120
QY	121	QMSNLRAEDTAVVYCAKILLAGRGWYFDLMGKGTPTVYSSGGGSGSGGSGSSSELTQ	180
Db	121	QMSNLRAEDTAVVYCAKILLAGRGWYFDLMGKGTPTVYSSGGGSGSGGSGSSSELTQ	180
QY	181	DPAYSVALGQYVKTCCGDSLRSYTAASVYQKPRQAPLVYITGKNRPSGIDPREGSSS	240
Db	181	DPAYSVALGQYVKTCCGDSLRSYTAASVYQKPRQAPLVYITGKNRPSGIDPREGSSS	240
QY	241	GNTASLITTGAAQAEDEADYUCNSRDSGNNHVVFGGKTLVLGAADNNHNNHQAADQKLI	300
Db	241	GNTASLITTGAAQAEDEADYUCNSRDSGNNHVVFGGKTLVLGAADNNHNNHQAADQKLI	300
QY	301	SEEDLNGAA 309	
Db	301	SEEDLNGAA 309	

RESULT 2
 US-10-052-798-9
 Sequence 9, Application US/10052798
 Publication No. US20020150985A1
 GENERAL INFORMATION:
 APPLICANT: Adams, Camilla W.
 Ashkenazi, Avi J.
 Chuntcharapai, Anan
 Kim, Kyung J.
 TITLE OF INVENTION: Apo-2 Receptor
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/052,798
 FILING DATE: 02-NO. US20020150985A1-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/079,029
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:

```

1 NAME: Matschang, Diane L.
2 REGISTRATION NUMBER: 35,600
3 REFERENCE/DOCKET NUMBER: P1101R2
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 650/225-5416
6 TELEFAX: 650/952-9881
7
8 INFORMATION FOR SEQ ID NO: 9:
9
10 SEQUENCE CHARACTERISTICS:
11
12 LENGTH: 309 amino acids
13 TYPE: Amino Acid
14 TOPOLOGY: Linear
15
16 SEQUENCE DESCRIPTION: SEQ ID NO: 9:
17
18 US-10-052-798-9

```

Query Match	100.0%	Score 1633	DB 14	Length 309
Best Local Similarity	100.0%	Pred. No. 8	5e-108	
Matches 309	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	MMITPSSFGAFEEIENNVKKLLFALPLVPEFAAPAAAEVOLVOSGGVBERPGSRLS	60
Db	1	MMITPSSFGAFEEIENNVKKLLFALPLVPEFAAPAAAEVOLVOSGGVBERPGSRLS	60
QY	61	CAASGTFPDDYIGMSWYRQAPGKGLEWVSGINNGSGTADSVKGRVTISDNKNSLYL	120
Db	61	CAASGTFPDDYIGMSWYRQAPGKGLEWVSGINNGSGTADSVKGRVTISDNKNSLYL	120
QY	121	QMSLRAEDTAAYVYCAKILGAGRGMVFDLMGKGTITVYSSGGGSGGGSGGGSELTQ	180
Db	121	QMSLRAEDTAAYVYCAKILGAGRGMVFDLMGKGTITVYSSGGGSGGGSGGGSELTQ	180
QY	181	DPAVSALGQYVHTITCGDSLRSYYTASMYQCKPGCAPLVITYGKNRPSGIPDFSSSS	240
Db	181	DPAVSALGQYVHTITCGDSLRSYYTASMYQCKPGCAPLVITYGKNRPSGIPDFSSSS	240
QY	241	GNPASTLTITGAQAEDEADYYCNSRPSGNNHVFGGGKLTVLGAADNNHNNHGADEOKLI	300
Db	241	GNPASTLTITGAQAEDEADYYCNSRPSGNNHVFGGGKLTVLGAADNNHNNHGADEOKLI	300
QY	301	SEEDLINGAA 309	
Db	301	SEEDLINGAA 309	

RESULT 3
 US-10-288-917-10
 ; Sequence 10, Application US/10288917
 ; Publication No. US20030148453A1
 ; GENERAL INFORMATION:
 APPLICANT: Adams, Camilla W.
 Ashkenazi, Avi J.
 Chuntcharapai, Anan
 Kim, Kyung J.
 TITLE OF INVENTION: Apo-2 Receptor
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/288, 917
 FILING DATE: 06-No. US20030148453A1-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 10/052798
 FILING DATE: 02-NOV-2001

APPLICATION NUMBER: 09/079029
FILING DATE: 14-MAY-1998
APPLICATION NUMBER: 60/074119
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 60/046615
FILING DATE: 15-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-288-917-10

Query Match 89.4%; Score 1460.5; DB 12; Length 312;
Best Local Similarity 90.1%; Pred. No. 1.2e-95;
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;
QY 1 MTMTSPGAFLEIFNVKLLFAIPLVYFYFAADPAMAEVOLVOSGGVRRPGSLRLS 60
DB 1 MTMTSPGAFLEIFNVKLLFAIPLVYFYFAADPAMAGVOLVBSGGGLVDPGSLRLS 60
QY 61 CAASGTFDDYGMWVQRAPGKGLGVNSGINNGSGTGYADSVKGRVTISRDNKNSLYL 120
DB 61 CAASGTFESSYMWQRAPGKGLGVNSGINNGSGTGYADSVKGRVTISRDNKNSLYL 120
QY 121 QNNSLRAPETAVYYCA---KILGAGRGVFDLMKGTIVTVYSSGGSGSGSGSGSS 176
DB 121 QNNSLRAPETAVYYCARDLLKYGSSSGW-FDPWGRGTIVTVYSSGGSGSGSGSGSS 179
QY 177 ELTOPAVVALGQVYRITCGDLSRSYASWYQKPGQAPVLYTGKNNRPSGIPDRS 236
DB 180 ELTOPAVVALGQVYRITCGDLSRSYASWYQKPGQAPVLYTGKNNRPSGIPDRS 239
QY 237 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGKLTLYLGAANHHNHGAAE 296
DB 240 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGKLTLYLGAANHHNHGAAE 299
QY 297 OKLISEEDLNGAA 309
DB 300 OKLISEEDLNGAA 312

RESULT 4
US-10-052-798-10
Sequence 10, Application US/10052798
Publication No. US20020150985A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
Ashkenazi, Avi J.
Chuntharapai, Anan
Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/052,798
FILING DATE: 02-NO. US20020150985A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-052-798-10

Query Match 89.4%; Score 1460.5; DB 14; Length 312;
Best Local Similarity 90.1%; Pred. No. 1.2e-95;
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;
QY 1 MTMTSPGAFLEIFNVKLLFAIPLVYFYFAADPAMAEVOLVOSGGVRRPGSLRLS 60
DB 1 MTMTSPGAFLEIFNVKLLFAIPLVYFYFAADPAMAGVOLVBSGGGLVDPGSLRLS 60
QY 61 CAASGTFDDYGMWVQRAPGKGLGVNSGINNGSGTGYADSVKGRVTISRDNKNSLYL 120
DB 61 CAASGTFESSYMWQRAPGKGLGVNSGINNGSGTGYADSVKGRVTISRDNKNSLYL 120
QY 121 QNNSLRAPETAVYYCA---KILGAGRGVFDLMKGTIVTVYSSGGSGSGSGSGSS 176
DB 121 QNNSLRAPETAVYYCARDLLKYGSSSGW-FDPWGRGTIVTVYSSGGSGSGSGSGSS 179
QY 177 ELTOPAVVALGQVYRITCGDLSRSYASWYQKPGQAPVLYTGKNNRPSGIPDRS 236
DB 180 ELTOPAVVALGQVYRITCGDLSRSYASWYQKPGQAPVLYTGKNNRPSGIPDRS 239
QY 237 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGKLTLYLGAANHHNHGAAE 296
DB 240 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGKLTLYLGAANHHNHGAAE 299
QY 297 OKLISEEDLNGAA 309
DB 300 OKLISEEDLNGAA 312

RESULT 5
US-10-288-917-11
Sequence 11, Application US/10288917
Publication No. US20030148455A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
Ashkenazi, Avi J.
Chuntharapai, Anan
Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/288.917
  FILING DATE: 06-Nov-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 10/052798
  FILING DATE: 02-Nov-2001
  APPLICATION NUMBER: 09/079029
  FILING DATE: 14-May-1998
  APPLICATION NUMBER: 60/074119
  FILING DATE: 09-Feb-1998
  APPLICATION NUMBER: 60/046615
  FILING DATE: 15-May-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Marschang, Diane L.
  REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2D1C1
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650/225-5416
  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 310 amino acids
    TYPE: Amino Acid
    TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-288-917-11
```

```
Query Match      75.4%; Score 1231.5; DB 12; Length 310;
Best Local Similarity 78.0%; Pred. No. 1.7e-79;
Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

QY 1 MMTITPSFGAFLEINNVKKLLEFAIPLVVPEYAAOPAMAEVOLVOSGGVERGSGSLRLS 60
   1 MMTITPSFGAFLEINNVKKLLEFAIPLVVPEYAAOPAMAEVOLVOSGGVVGGRSLRLS 60
Db 1 MMTITPSFGAFLEINNVKKLLEFAIPLVVPEYAAOPAMAEVOLVOSGGVVGGRSLRLS 60

QY 61 CAASGFTFDYGSWVRQAPKGLKLEWVSGINMGSGTGYADSVKGRVTISRDNKNSLYL 120
   61 CAASGFTFSSYGHMVRQAPKGLKLEWVAGIFDGKKNKYADSVKGRFTISRDNKNTLYL 120
Db 61 CAASGFTFSSYGHMVRQAPKGLKLEWVAGIFDGKKNKYADSVKGRFTISRDNKNTLYL 120

QY 121 QMNSLRAEDTAVYYCAKILGAGRGWTF-DLMGKGTIVTVSSGGGSGGGSGGGG-SEL 178
   121 QMNSLRAEDTAVYYCAR---DRGYIYMDVMGKGTIVTVSSGGGSGGGSGGGGQSQSVL 176
Db 121 QMNSLRAEDTAVYYCAR---DRGYIYMDVMGKGTIVTVSSGGGSGGGSGGGGQSQSVL 176

QY 179 TOPPAVSVALGQVTRTCOGDSLRL---SYAASWYQOKPGQAPVLYTVGKNNRPSGIPDRF 235
   179 TOPPAVSVALGQVTRTCOGDSLRL---SYAASWYQOKPGQAPVLYTVGKNNRPSGIPDRF 235
Db 179 TOPPAVSVALGQVTRTCOGDSLRL---SYAASWYQOKPGQAPVLYTVGKNNRPSGIPDRF 235

QY 236 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLGAAGAAHHHHHGAA 295
   236 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLGAAGAAHHHHHGAA 295
Db 236 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLGAAGAAHHHHHGAA 295

QY 296 EOKLISEEDLNGAA 309
   296 EOKLISEEDLNGAA 309
Db 296 EOKLISEEDLNGAA 309
```

```
RESULT 6
US-10-052-798-11
Sequence 11, Application US/10052798
Publication No. US20020150985A1
GENERAL INFORMATION:
  APPLICANT: Adams, Camilla W.
              Ashkenazi, Avi J.
              Chuntharapai, Anan
              Kim, Kyung J.
  TITLE OF INVENTION: Apo-2 Receptor
  NUMBER OF SEQUENCES: 14
  CORRESPONDENCE ADDRESSES:
    ADDRESSEE: Genentech, Inc.
    STREET: 1 DNA Way
    CITY: South San Francisco
```

```
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
  MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/052.798
  FILING DATE: 02-Nov-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/079.029
  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
  NAME: Marschang, Diane L.
  REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650/225-5416
  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 310 amino acids
    TYPE: Amino Acid
    TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-052-798-11
```

```
Query Match      75.4%; Score 1231.5; DB 14; Length 310;
Best Local Similarity 78.0%; Pred. No. 1.7e-79;
Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

QY 1 MMTITPSFGAFLEINNVKKLLEFAIPLVVPEYAAOPAMAEVOLVOSGGVERGSGSLRLS 60
   1 MMTITPSFGAFLEINNVKKLLEFAIPLVVPEYAAOPAMAEVOLVOSGGVVGGRSLRLS 60
Db 1 MMTITPSFGAFLEINNVKKLLEFAIPLVVPEYAAOPAMAEVOLVOSGGVVGGRSLRLS 60

QY 61 CAASGFTFDYGSWVRQAPKGLKLEWVSGINMGSGTGYADSVKGRVTISRDNKNSLYL 120
   61 CAASGFTFSSYGHMVRQAPKGLKLEWVAGIFDGKKNKYADSVKGRFTISRDNKNTLYL 120
Db 61 CAASGFTFSSYGHMVRQAPKGLKLEWVAGIFDGKKNKYADSVKGRFTISRDNKNTLYL 120

QY 121 QMNSLRAEDTAVYYCAKILGAGRGWTF-DLMGKGTIVTVSSGGGSGGGSGGGG-SEL 178
   121 QMNSLRAEDTAVYYCAR---DRGYIYMDVMGKGTIVTVSSGGGSGGGSGGGGQSQSVL 176
Db 121 QMNSLRAEDTAVYYCAR---DRGYIYMDVMGKGTIVTVSSGGGSGGGSGGGGQSQSVL 176

QY 179 TOPPAVSVALGQVTRTCOGDSLRL---SYAASWYQOKPGQAPVLYTVGKNNRPSGIPDRF 235
   179 TOPPAVSVALGQVTRTCOGDSLRL---SYAASWYQOKPGQAPVLYTVGKNNRPSGIPDRF 235
Db 179 TOPPAVSVALGQVTRTCOGDSLRL---SYAASWYQOKPGQAPVLYTVGKNNRPSGIPDRF 235

QY 236 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLGAAGAAHHHHHGAA 295
   236 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLGAAGAAHHHHHGAA 295
Db 236 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLGAAGAAHHHHHGAA 295

QY 296 EOKLISEEDLNGAA 309
   296 EOKLISEEDLNGAA 309
Db 296 EOKLISEEDLNGAA 310
```

```
RESULT 7
US-09-880-748-2038
Sequence 2038, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
  APPLICANT: Ruben et al.
  TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys
  FILE REFERENCE: PF523
  CURRENT APPLICATION NUMBER: US/09/880.748
  CURRENT FILING DATE: 2001-06-15
  PRIOR APPLICATION NUMBER: 60/212.210
  PRIOR FILING DATE: 2000-06-15
  PRIOR APPLICATION NUMBER: 60/240.816
  PRIOR FILING DATE: 2000-10-17
```

;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 2038
;; LENGTH: 239
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-2038

Query Match 73.1%; Score 1194.5; DB 11; Length 239;
Best Local Similarity 93.4%; Pred. No. 5.4e-77;
Matches 228; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

QY 40 EVOLVOSGGGVERPGGSLRLSCAASGFTFDDYGMSSVVRQAPGKLEWVSGIMNNGSGTGY 99
|||||
Db 1 EVOLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSSVVRQAPGKLEWVSGIMNNGSGTGY 60
QY 100 ADSVKGRTISRDNAKNSLYLQMNSLRAEDTAVYCAKILGARGVYFDLMKGTIVTVS 159
|||||
Db 61 ADSVKGRTISRDNAKNSLYLQMNSLRAEDTAVYCAR-----RRALDYWGQGLTVTVS 115
QY 160 SGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYASVYQKPGQAPVL 219
|||||
Db 116 SGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYASVYQKPGQAPVL 175
QY 220 VIYKNNRPSGIPDRFSGSSSGNTASLITGAQAEDEADYYCNSRDSGHNHVFVGGTKL 279
|||||
Db 176 VIYKNNRPSGIPDRFSGSSSGNTASLITGAQAEDEADYYCNSRDSGHNHVFVGGTKL 235
QY 280 TVLG 283
|||||
Db 236 TVLG 239

RESULT 8
US-09-880-748-937
;; Sequence 937, Application US/09880748
;; Publication No. US20030059937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 937
;; LENGTH: 239
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-937

Query Match 72.8%; Score 1189.5; DB 11; Length 239;
Best Local Similarity 93.0%; Pred. No. 1.2e-76;
Matches 227; Conservative 4; Mismatches 8; Indels 5; Gaps 1;
QY 40 EVOLVOSGGGVERPGGSLRLSCAASGFTFDDYGMSSVVRQAPGKLEWVSGIMNNGSGTGY 99
|||||

Db 1 EVOLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSSVVRQAPGKLEWVSGIMNNGSGTGY 60
QY 100 ADSVKGRTISRDNAKNSLYLQMNSLRAEDTAVYCAKILGARGVYFDLMKGTIVTVS 159
|||||
Db 61 ADSVKGRTISRDNAKNSLYLQMNSLRAEDTAVYCAR-----RRALDYWGQGLTVTVS 115
QY 160 SGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYASVYQKPGQAPVL 219
|||||
Db 116 SGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYASVYQKPGQAPVL 175
QY 220 VIYKNNRPSGIPDRFSGSSSGNTASLITGAQAEDEADYYCNSRDSGHNHVFVGGTKL 279
|||||
Db 176 VIYKNNRPSGIPDRFSGSSSGNTASLITGAQAEDEADYYCNSRDSGHNHVFVGGTKL 235
QY 280 TVLG 283
|||||
Db 236 TVLG 239

RESULT 9
US-09-880-748-2015
;; Sequence 2015, Application US/09880748
;; Publication No. US20030059937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 2015
;; LENGTH: 239
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-2015

Query Match 72.2%; Score 1178.5; DB 11; Length 239;
Best Local Similarity 91.8%; Pred. No. 7.3e-76;
Matches 224; Conservative 7; Mismatches 8; Indels 5; Gaps 1;

QY 40 EVOLVOSGGGVERPGGSLRLSCAASGFTFDDYGMSSVVRQAPGKLEWVSGIMNNGSGTGY 99
|||||
Db 1 EVOLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSSVVRQAPGKLEWVSGIMNNGSGTGY 60
QY 100 ADSVKGRTISRDNAKNSLYLQMNSLRAEDTAVYCAKILGARGVYFDLMKGTIVTVS 159
|||||
Db 61 ADSVKGRTISRDNAKNSLYLQMNSLRAEDTAVYCAR-----RRALDYWGQGLTVTVS 115
QY 160 SGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYASVYQKPGQAPVL 219
|||||
Db 116 SGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYASVYQKPGQAPVL 175
QY 220 VIYKNNRPSGIPDRFSGSSSGNTASLITGAQAEDEADYYCNSRDSGHNHVFVGGTKL 279
|||||
Db 176 VIYKNNRPSGIPDRFSGSSSGNTASLITGAQAEDEADYYCNSRDSGHNHVFVGGTKL 235
QY 280 TVLG 283
|||||
Db 236 TVLG 239

RESULT 10

```
US-09-880-748-2013
; Sequence 2013, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2013
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2013

Query Match          69.7%; Score 1139; DB 11; Length 240;
Best Local Similarity 89.3%; Pred. No. 4,5e-73;
Matches 218; Conservative 10; Mismatches 12; Indels 4; Gaps 1;

QY 40 EVOLVSGGVERPGSLRLSCAASGFTPDYGMVNRQAPGKLEWVSGINMGSTGY 99
   :|||||: :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSYINSGSTYY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 100 ADVKGRVITSRNANKSLYLQNNSLRAEDTAVYCAKILIGARGWTFDLMGKTYTVS 159
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADVKGRFTISRANKSKTLYLQNNSLRAEDTAVYCAKLV---KRYFDWGGKTVTAS 116
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 160 SGGGSGGGSGGSGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVL 219
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 SGGGSGGGSGGSGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVL 176
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 220 VITGKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYICNSRSSGHHVFGGQTKL 279
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 VITGKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYICNSRSSGHHVFGGQTKL 236
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 280 TVLG 283
   :|||||:
Db 237 TVLG 240
   :|||||:

RESULT 11
US-09-880-748-1416
; Sequence 1416, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
```

```
SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1416
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1416

Query Match          69.7%; Score 1138; DB 11; Length 252;
Best Local Similarity 86.9%; Pred. No. 5,5e-73;
Matches 219; Conservative 11; Mismatches 14; Indels 8; Gaps 2;

QY 40 EVOLVSGGVERPGSLRLSCAASGFTPDYGMVNRQAPGKLEWVSGINMGSTGY 99
   :|||||: :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVSGGGLVQPGSLRLSCAASGFTPEDEAMHVRQAPGKLEWVSGISINSGSIAY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 100 ADVKGRVITSRNANKSLYLQNNSLRAEDTAVYCAKILG-----AGRWTF--DLWG 151
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADVKGRFTISRANKSLYLQNNSLRAEDTAVYCAKIRGVYDILTRTYGGDWVG 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 152 KGTTVTVSSGGGGSGGSGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQ 211
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 QRTMTVTVSSGGGGSGGSGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQ 180
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 212 KPGQAPVLYLYGKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYICNSDSSGNNY 271
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 KPGQAPVLYLYGKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYICNSDSSGNNY 240
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 272 VFGGQTKLTVLG 283
   :|||||:|||||:
Db 241 VFGGQTKLTVLG 252
   :|||||:|||||:

RESULT 12
US-09-969-748C-2
; Sequence 2, Application US/09969748C
; Publication No. US20030161809A1
; GENERAL INFORMATION:
; APPLICANT: ARIZERA PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLYNN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; APPLICANT: BASU, Anatesh
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACT
; FILE REFERENCE: 057220-0303
; CURRENT APPLICATION NUMBER: US/09/969,748C
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-748C-2

Query Match          69.1%; Score 1129; DB 12; Length 290;
Best Local Similarity 80.1%; Pred. No. 2,8e-72;
Matches 226; Conservative 18; Mismatches 20; Indels 18; Gaps 4;

QY 33 AAQPAMA-----EVOLVSGGVERPGSLRLSCAASGFTPDYGMVNRQAPGKLEWV 87
   :|||||: :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 16 AAQPAMADYKAKOVOLVSGGGLVQPGSLRLSCAASGFTFSYAMHVRQAPGKLEWV 75
```

RESULT 14
US-09-880-748-2023
: Sequence: 2023, Application US/09880748
: Publication No. US20030059937A1
: GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: Antbodies that Immunospecifically Bind BlyS
: FILE REFERENCE: pf523
: CURRENT APPLICATION NUMBER: US/09/880.748

```

/ RESULT 15
/ US-09-969-748C-12
/ Sequence 12, Application US/09969748C
/ Publication No. US20030161809A1
/ GENERAL INFORMATION:
/ APPLICANT: ARIZERE PHARMACEUTICALS, INC.
/ APPLICANT: HOUSTON, Lou, L.
/ APPLICANT: SHERIDAN, Philip, J.
/ APPLICANT: HAWLEY, Stephen
/ APPLICANT: GUYNN, Jacqueline, M.
/ APPLICANT: CHAPIN, Steven
/ APPLICANT: BASU, Amarendra
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CELLULAR BARRIERS
/ TITLE OF INVENTION: AGENTS ACROSS CELLULAR BARRIERS
/ FILE REFERENCE: 057220-0303
/ CURRENT APPLICATION NUMBER: US/09/969,748C
/ CURRENT FILING DATE: 2002-12-10
/ PRIOR APPLICATION NUMBER: US 60/267,601
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: US 60/248,819
/ PRIOR FILING DATE: 2000-11-14
/ PRIOR APPLICATION NUMBER: US 60/248,478
/ PRIOR FILING DATE: 2000-11-13
/ PRIOR APPLICATION NUMBER: US 60/237,929
/ PRIOR FILING DATE: 2000-10-02
/ NUMBER OF SEQ ID NOS: 115
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 12
/ LENGTH: 296

```

TYPE: PRT
ORGANISM: Homo sapiens
US-09-969-748C-12

Query Match 68.7%; Score 1122; DB 12; Length 296;
Best Local Similarity 79.8%; Pred. No. 8 Be-72;
Matches 225; Conservative 18; Mismatches 27; Indels 12; Gaps 4;

```
OY      33 AAQPAMA---EVLVDSGGGVERPFGSLRLSCAASGFTFDDYGMWVROAPGKGLEWV 87
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      16 AAQPAMADYKAKQVQLVDSGGGVDPGRSLRLSCAASGFTFSSYAMHWVROAPGKLEWV 75
OY      88 SGINMGSGTGADSYKGRVTISRDNAKNSLYLQMNSLRAEDTAYYYCAKILGAGRWYF 147
      | |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      76 SAISGSGSGTYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAYYYCAR--DTRG-YF 131
OY      148 DLMGKGTVTYVSSGGGSGGSGGSSSELTQDPAVSYALGOTVRITCGDPLRSYAS 207
      |||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      132 DLMGKGTLYTVSSGGGSGGSGGSGGSSSELTQDPAMSYALGOTVRITCGDPLRKYHAS 191
OY      208 WYQQRPGQAPVLYVYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADADYYCNSRDS 267
      |||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      192 WYQQRPRQAPRLVYVGKNERPSGIPDRFSGSTSGPTASLTISGLQAEDEADADYYCHSRDSN 251
OY      268 GHHVYFSGGSKTLTVGAHAHHHHHGAAPQKLISEDLNGAA 309
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      252 ADLVVFGGSKTVYLVGGG--GSCAAAEQKLISEDLNGAA 290
```

Search completed: September 22, 2003, 15:36:23
Job time : 35.1858 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 20.9098 Seconds
(without alignments)
1421.159 Million cell updates/sec

Title: US-10-052-798-9
Perfect score: 1633
Sequence: 1 MTMTSPFGAFLEIFNVKK.....HHGAPQKLISEEDLNGAA 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	720	44.1	268	2 A56446	Ig heavy chain V r
2	571.5	35.0	249	2 S41374	single chain Fv an
3	568	34.8	109	2 S19663	Ig lambda chain V
4	562	34.4	108	2 S47184	Ig lambda chain -
5	551.5	33.8	110	2 S36272	Ig lambda chain V
6	546	33.4	121	2 S31104	Ig heavy chain (su
7	546	33.4	127	2 S70444	Ig lambda chain pr
8	541	33.1	108	2 S38498	Ig lambda chain -
9	539	33.0	109	2 S38498	Ig lambda chain -
10	531.5	32.5	233	2 JC5322	p53 specific singl
11	530	32.5	233	2 S25748	Ig lambda chain -
12	527	32.3	108	1 L3HUSH	Ig lambda chain V
13	518.5	31.8	110	2 S19672	Ig lambda chain V
14	517.5	31.7	146	2 S02083	Ig lambda chain V
15	509	31.2	123	2 S30532	Ig heavy chain V r
16	503.5	30.8	128	2 S31595	Ig heavy chain V r
17	503	30.8	96	2 S36060	Ig lambda chain -
18	503	30.8	115	2 S13726	Ig lambda chain V
19	503	30.8	120	2 S36273	Ig heavy chain V r
20	503	30.8	121	2 S31118	Ig heavy chain - h
21	502	30.7	138	2 S31666	Ig heavy chain - h
22	502	30.7	233	2 S25741	Ig lambda chain V
23	498.5	30.5	120	2 S44111	Ig heavy chain V-D
24	498	30.5	119	2 S31107	Ig heavy chain - h
25	494	30.3	98	2 S26928	Ig heavy chain V r
26	492	30.1	119	2 C36005	Ig heavy chain V r
27	491.5	30.1	128	2 S26790	Ig heavy chain V r
28	491	30.1	160	2 S05271	Ig heavy chain pre
29	489.5	30.0	112	2 PH1654	Ig heavy chain V r

30	488.5	29.9	145	2 S11239	Ig heavy chain V r
31	485	29.7	140	2 S31686	Ig heavy chain V r
32	482.5	29.5	120	2 S48798	Ig heavy chain V r
33	482	28.5	123	2 S31114	Ig heavy chain - h
34	481	28.5	119	2 D36005	Ig heavy chain V r
35	480.5	29.4	140	2 S70442	Ig heavy chain pre
36	480	29.4	121	2 S19666	Ig heavy chain V r
37	480	29.4	140	2 S31588	Ig heavy chain V r
38	479.5	29.4	147	2 S17780	Ig variable region
39	476	29.1	119	2 S31108	Ig heavy chain - h
40	473	29.0	127	2 S38489	Ig heavy chain - h
41	470.5	28.8	141	2 S31105	Ig heavy chain (su
42	470.5	28.8	118	2 S31669	Ig heavy chain V r
43	469.5	28.8	120	2 E49590	Ig heavy chain V r
44	469	28.7	120	2 S36278	Ig heavy chain V r
45	468	28.7	121	2 I55673	Ig heavy chain - h

ALIGNMENTS

RESULT 1
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C:Species: Mus musculus (house mouse)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C:Accession: A56446
R:Yang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A:Title: A high affinity disgonin-binding protein displayed on M13 is functionally ide
A:Reference number: A56446; MUID:95229583; PMID:7713873
A:Accession: A56446
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-268 <TAN>
A:Cross-references: GB:U20617
C:Keywords: heterotetramer; immunoglobulin

Query Match 44.1%; Score 720; DB 2; Length 268;
Best Local Similarity 53.6%; Pred. No. 5.3e-41;
Matches 147; Conservative 38; Mismatches 81; Indels 8; Gaps 5;

QY	38	MAEVLVDSGGGVERPGSLRLSCAASGFTPDYGMVWROAPKGLMEVIMNGGST	97
DB	1	MAQVKLQESGAELVYKPGASVKLTCTGSPFNKIDTYMHVKKQRPDGLMIGHRIAPANGIT	60
QY	98	GYADSVKGRVITISRDNAKNSLYLQNNSLRAEDTAVYCAKILGAGRGVYFDLMGKGTIVT	157
DB	61	KYDPKFGQKATIAADTSSNFAVLQLSLTSEDTAVYCYASYLFR--YENVWGQGTIVT	117
QY	158	VSSGGGSGGGSGGGSGSS-ELTDPNAV-SVALGQTVRITQGDLSRYVASMVOOKRGO	215
DB	118	VSSGGGSGGGSGGGSGGSDIELTQSPALMSASLGGKVMSCRASSSVN-FLYVWQOKKDA	176
QY	216	APLVITYKNNRPSSGIPRFGSSSGNPTASLTITGAQEDADYVACNSRDSGNHVPVG	275
DB	177	SPKLWVYTTSHLPREVPRPFRSGSGSGNYSLTISMEBEDATYTCQQTSS--PFTTGS	234
QY	276	GTKLITVLGAHAHHHHHNGAEOKLISEEDLNGAA	309
DB	235	GTKLEIKRSAHHHHHNGAEOKLISEEDLNGAA	268

RESULT 2
S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv anti

A:Accession: S41374
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:Z29480

Query Match 35.0%; Score 571.5; DB 2; Length 249;
Best Local Similarity 48.3%; Pred. No. 3.8e-31;
Matches 125; Conservative 38; Mismatches 73; Indels 23; Gaps 7;

QY 40 EVOLVGGGVEPESLRLSCAAGFTDDYCGMSVVRAPGKGLGSGINNGSTG 99
DB 1 QVQLDQSGAEIVRGVSGVLRSCASGPNKRDYIHVWQKPEKGLMIARIAPASGVK 60
QY 100 ADSVKRVTISRDNANSLYLQWNSLRAPEDAVYYCAK--ILAGRWYFDLWGKGTVA 157
DB 61 VPRFQKARTITADTSSNTAVYLLSLTSEDTAVYCARNDLTLSLGY----WGQSTVA 116
QY 158 VSSGGGGSGGGGGGGSS-ELTQD-PANVALGQVTRITCQ-----GDSLRSYA 206
DB 117 VSSRGGGSGGGGGSGSDIELTQSPSVVYIPGESVISICRSKSLYSXSDGS---YL 172
QY 207 SWYQKPGQAPVYVIRGKNNRPSGIDPRFGSSSGMTASLTITGAQAEDEADYCNRS 266
DB 173 FFWLQRPQSPOLLITRMNSLASGVDPDRFGSGSGTSFTLRISVEEDVGYTCMQHRE 232
QY 267 SGNHVVEGGGKTLTVLGAA 285
DB 233 --YPLTFAGATKLEKRAA 249

RESULT 3

Ig lambda chain V region (clone alpha-B8A3) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19663
R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A>Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage
A:Reference number: S19663; MID:92085276; PMID:1748994
A:Accession: S19663
A:Molecule type: mRNA
A:Residues: 1-109 <MAR>
A:Cross-references: EMBL:X61640; NID:929492; PIDN:CAA43821.1; PID:91340166
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 34.8%; Score 568; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.8e-31;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 SSELTDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLYTYGKNNRPSGIPDR 234
DB 1 SSELTDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLYTYGKNNRPSGIPDR 60
QY 235 FSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFEGGKTLTVLG 283
DB 61 FSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFEGGKTLTVLG 109

RESULT 4

Ig lambda chain - human
S47184
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S47184
R:McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
A>Note: the EMBL Data Library, June 1994
A:Description: Cloning and analysis of Igm anti-thyroglobulin autoantibodies from patient
A:Reference number: S47181
A:Accession: S47184

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <MC1>
A:Cross-references: EMBL:X79783; NID:9506446; PIDN:CAA56179.1; PID:9506427
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 34.4%; Score 562; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 6.9e-31;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 SSELTDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLYTYGKNNRPSGIPDR 234
DB 1 SSELTDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLYTYGKNNRPSGIPDR 60
QY 235 FSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFEGGKTLTVL 282
DB 61 FSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFEGGKTLTVL 108

RESULT 5

Ig lambda chain V region (clone alpha-THY-29) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36272
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMO J. 12, 725-734, 1993
A>Title: Human anti-self antibodies with high specificity from phage display library
A:Reference number: S36256; MID:93178448; PMID:7679990
A:Accession: S36272
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-110 <GR1>
A:Cross-references: EMBL:Z18833; NID:933419; PIDN:CAA79285.1; PID:9939912
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 33.8%; Score 551.5; DB 2; Length 110;
Best Local Similarity 98.2%; Pred. No. 3.5e-30;
Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 175 SSELTDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLYTYGKNNRPSGIPDR 234
DB 1 SSELTDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLYTYGKNNRPSGIPDR 60
QY 235 FSGSSSGNTASLTITGAQAEDEADYCNRSRDSGN-HVFFGGGKTLTVLG 283
DB 61 FSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNLVVFGGKTLTVLG 110

RESULT 6

Ig heavy chain (subclass IgM) - human (fragment)
S31104
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S31104
R:Raaporst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur Eut. J. Immunol. 22, 247-251, 1992
A>Title: Restricted utilization of germ-line VH3 genes and short diverse third comp
A:Reference number: S31104; MID:92111633; PMID:1730252
A:Accession: S31104
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <RAA>
A:Cross-references: EMBL:X63080; NID:932646; PIDN:CAA44802.1; PID:932647
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>


```
Query Match          33.4%; Score 546; DB 2; Length 121;
Best Local Similarity 84.3%; Pred. No. 9e-30;
Matches 102; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 40 EQVLQSGGVRPGSLRLSCAASGFTFDYGMASVWQAQAPKGLLEWYSGIMWNGSGITCY 99
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EQVLQSGGGLVQAPRSRLSCAASGFTFDYAMHWQAQAPKGLLEWYSGISWNGSGITCY 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 100 ADVVGRVYISRDNKNLSLYLQMSLRADFTAVYVYCAKILGAGRGVYFDLMGKGTPTVYS 159
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADVVGRVYISRDNKNLSLYLQMSLRADFTALYICADVFGSGVTFDLMGKGLTVYS 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 160 S 160
      |
Db 121 S 121

RESULT 7
S70444
Ig lambda chain precursor V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C:Accession: S70444; S70426
R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A:Title: Igm kappa/lambda EBV human B cell clone: an early step of differentiation of fe
A:Reference number: S70442; MUID:93024508; PMID:1383695
A:Accession: S70444
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-127 <CUI>
A:Experimental source: clone E29.1
submitted to the EMBL Data Library, May 1990
A:Reference number: S70426
A:Accession: S70426
A:Molecule type: mRNA
A:Residues: 1-90 <TON>
A:Cross-references: EMBL:X53070
A:Experimental source: cell line E29.1, clone VL 29-1
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:1-20/Domain: signal sequence status predicted <SIG>
F:1-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>
F:34-108/Domain: Immunoglobulin homology <IMM>

Query Match          33.4%; Score 546; DB 2; Length 127;
Best Local Similarity 97.2%; Pred. No. 9.4e-30;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 175 SSELQDPAVSVALGQTVRTTCGDSLRSYVSWYQKPGQAPVLVYTKNNRPSGIPDR 234
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 SSELQDPAVSVALGQTVRTTCGDSLRSYVSWYQKPGQAPVLVYTKNNRPSGIPDR 79
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 235 FSGSSGNFASLTITGAQAEADADYYCNSRDSGNHNVFGGKTLTVL 282
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 FSGSSGNFASLTITGAQAEADADYYCNSRDSGNHNVFGGKTLTVL 127
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
S38498
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S38498
R:Maris, J.D.; Ouwehand, W.H.; Bye, J.M.; Finneer, R.; Gorlick, B.D.; Voak, D.; Thorpe, S
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a H
A:Reference number: S38488
A:Accession: S38498
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <MAR>
```

```
A:Cross-references: EMBL:Z23035; NID:9414043; PIDN:CA80570.1; PID:9414044
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:14-88/Domain: Immunoglobulin homology <IMM>

Query Match          33.1%; Score 541; DB 2; Length 108;
Best Local Similarity 97.2%; Pred. No. 1.7e-29;
Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 176 SSELQDPAVSVALGQTVRTTCGDSLRSYVSWYQKPGQAPVLVYTKNNRPSGIPDR 235
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 SSELQDPAVSVALGQTVRTTCGDSLRSYVSWYQKPGQAPVLVYTKNNRPSGIPDR 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 236 SGGSSGNFASLTITGAQAEADADYYCNSRDSGNHNVFGGKTLTVL 283
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SGGSSGNFASLTITGAQAEADADYYCNSRDSGNHNVFGGKTLTVL 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
S38496
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S38496
R:Maris, J.D.; Ouwehand, W.H.; Bye, J.M.; Finneer, R.; Gorlick, B.D.; Voak, D.; Thorpe
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from
A:Reference number: S38488
A:Accession: S38496
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <MAR>
A:Cross-references: EMBL:Z23031; NID:9414039; PIDN:CA80566.1; PID:9414040
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:15-89/Domain: Immunoglobulin homology <IMM>

Query Match          33.0%; Score 539; DB 2; Length 109;
Best Local Similarity 93.6%; Pred. No. 2.4e-29;
Matches 102; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 175 SSELQDPAVSVALGQTVRTTCGDSLRSYVSWYQKPGQAPVLVYTKNNRPSGIPDR 234
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 SSELQDPAVSVALGQTVRTTCGDSLRSYVSWYQKPGQAPVLVYTKNNRPSGIPDR 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 235 FSGSSGNFASLTITGAQAEADADYYCNSRDSGNHNVFGGKTLTVL 283
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FSGSSGNFASLTITGAQAEADADYYCNSRDSGNHNVFGGKTLTVL 109
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
JC5322
p53 specific single-chain antibody pab421 - human
C:Species: Homo sapiens (man)
C>Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R:Janot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MUID:97168950; PMID:9016757
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
A:Experimental source: hybridoma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It resto

Query Match          32.5%; Score 531.5; DB 2; Length 233;
Best Local Similarity 48.0%; Pred. No. 1.6e-28;
Matches 117; Conservative 34; Mismatches 74; Indels 19; Gaps 8;

OY 45 QSGGVRPGSLRLSCAASGFTFDYGMASVWQAQAPKGLLEWYSGIMWNGSGITVDSK 104
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ESGAEIVRSGASVKSCTTSGFNINDYHWHVKKRPEQGLEWIGRIDPENGADMRSSG 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```


Db 61 SSSSGNTASLTITGARAEDADYCNSSRNSSGNVHYFGGFKTLTVL 108

RESULT 15

S30532

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996

C:Accession: S30532

R:Marlette, X.

submitted to the EMBL Data Library, October 1992

A:Reference number: S30520

A:Accession: S30532

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-123 <MARK>

A:Cross-references: EMBL:Z18318

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 31.2%; Score 509; DB 2; Length 123;

Best Local Similarity 78.9%; Pred. No. 2.6e-27;

Matches 97; Conservative 8; Mismatches 16; Indels 2; Gaps 1;

```

OY 40 EVOLVSGGVEPRPGSLRLSCAASGFTEDDYGMWVRQAPGKGLEWYSGINMGSTGY 99
    |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGLVQPERGSRRLSCAASGFTEDDYAMHWVRQAPGKGLEWYSGISWNSGTLGY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 100 ADSVKGRVTISRDNKNSLYLQMSLRAEDTAVVYCAKILGAGRGW--YFDLWGKGTVT 157
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFAISRDNKNSLYLQMSLRAEDTALYCAKDTPYSSGWSNAFDIMWGCTMYT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 158 VSS 160
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 VSS 123
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Search completed: September 22, 2003, 15:14:58
 Job time : 21.9098 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:03 ; Search time 11.6165 Seconds
(without alignments)
1250.910 Million cell updates/sec

Title: US-10-052-798-9
Perfect score: 1633
Sequence: 1 MTMTSPSGAFLEIFNVK.....HHGAAGQKISEEDLNCA 309

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	527	32.3	108	LV3A_HUMAN	P01714 homo sapien
2	437.5	26.8	116	HV3T_HUMAN	P01781 homo sapien
3	436	26.7	115	HV3F_HUMAN	P01767 homo sapien
4	429	26.3	117	HV3C_HUMAN	P01764 homo sapien
5	428	26.2	121	HV3J_HUMAN	P01771 homo sapien
6	424.5	26.0	120	HV3Q_HUMAN	P01782 homo sapien
7	424.5	26.0	122	HV3G_HUMAN	P01768 homo sapien
8	422.5	25.9	114	HV3B_HUMAN	P01763 homo sapien
9	419	25.7	115	HV3D_HUMAN	P01765 homo sapien
10	413	25.3	119	HV3I_HUMAN	P01770 homo sapien
11	412.5	25.3	114	HV01_CANFA	P01784 canis famli
12	409.5	25.1	122	HV2I_MOUSE	P01790 mus musculu
13	408.5	25.0	119	HV3H_HUMAN	P01808 mus musculu
14	405.5	24.8	122	HV3H_HUMAN	P01769 homo sapien
15	404.5	24.8	122	HV2O_MOUSE	P01789 mus musculu
16	404	24.7	123	HV18_MOUSE	P01787 mus musculu
17	404	24.7	123	HV23_MOUSE	P01792 mus musculu
18	403	24.6	123	HV19_MOUSE	P01788 mus musculu
19	401.5	24.6	122	HV3A_HUMAN	P01762 homo sapien
20	401.5	24.6	136	HV16_MOUSE	P01783 mus musculu
21	399	24.4	123	HV22_MOUSE	P01794 mus musculu
22	397.5	24.3	116	HV05_CARAV	P01811 carassius a
23	396	24.2	123	HV24_MOUSE	P01793 mus musculu
24	395.5	24.2	126	HV3K_HUMAN	P01772 homo sapien
25	395	24.2	120	HV3E_HUMAN	P01776 homo sapien
26	391	23.9	119	HV3L_HUMAN	P01773 homo sapien
27	388	23.8	123	HV25_MOUSE	P01794 mus musculu
28	387.5	23.7	119	HV4O_MOUSE	P01810 mus musculu
29	384	23.5	117	HV54_MOUSE	P18525 mus musculu
30	382.5	23.4	119	HV37_MOUSE	P01807 mus musculu
31	382	23.4	117	HV55_MOUSE	P18526 mus musculu
32	382	23.4	118	HV39_MOUSE	P01809 mus musculu
33	380	23.3	117	HV02_CANFA	P01785 canis famli

34	380	23.3	144	HV26_MOUSE	P01795 mus musculu
35	377.5	23.1	119	HV3M_HUMAN	P01774 homo sapien
36	377	23.1	111	LV3B_HUMAN	P80748 homo sapien
37	376.5	23.1	97	HV56_MOUSE	P18527 mus musculu
38	375	23.0	117	HV4I_MOUSE	P01811 mus musculu
39	373.5	22.9	111	HV35_MOUSE	P01804 mus musculu
40	373.5	22.9	119	HV3N_HUMAN	P01775 homo sapien
41	373	22.8	115	HV32_MOUSE	P01801 mus musculu
42	372	22.8	98	HV57_MOUSE	P18528 mus musculu
43	372	22.8	107	LV4C_HUMAN	P01717 homo sapien
44	372	22.8	117	HV53_MOUSE	P18524 mus musculu
45	371.5	22.7	119	HV3P_HUMAN	P01777 homo sapien

ALIGNMENTS

RESULT 1	ID	LV3A_HUMAN	STANDARD:	PRT:	108 AA.
AC	P01714:	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Ig lambda chain V-II region SH.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=70166723; PubMed=4909564;				
RA	Titani K., Wikler M., Shinoda T., Putnam F.W.;				
RT	"The amino acid sequence of a lambda type Bence-Jones protein. 3. The				
RT	complete amino acid sequence and the location of the disulfide				
RT	bridges.";				
RL	J. Biol. Chem. 245:2171-2176(1970).				
CC	1- SIMILARITY: THIS IS A BENCE-JONES PROTEIN.				
CC	1- SIMILARITY: Contains 1 immunoglobulin-like domain.				
DR	PIR; A01980; L3HUSH.				
DR	HSSP; P80748; 2101.				
DR	GO; GO:0005576; C:extracellular; NAS.				
DR	GO; GO:0003823; F:antigen binding activity; NAS.				
DR	GO; GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; Igv; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
KW	Immunoglobulin V region; Bence-Jones protein.				
FT	DOMAIN 1 97				
FT	DISULFID 21 86				
FT	NON_TER 108 108				
SO	SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;				
Query Match	32.3%;	Score 527;	DB 1;	Length 108;	
Best Local Similarity	92.6%;	Pred. No. 2.4e-31;			
Matches 100;	Conservative	5;	Mismatches 3;	Indels 0;	Gaps 0;
QY	176	SELTDDPVSVVALGTVRTTCGDSLRSVYASWYQKFGQAAPVLYTYCKNNRPSGIPDRF	235		
DB	1	SELTDDPVSVVALGTVRTTCGDSLRSVYASWYQKFGQAAPVLYTYCKNNRPSGIPDRF	60		
OY	236	SGSSSGNTASLTITGAQAEDADYVCNSRDSSGNHVFEGGKTLTVLG	283		
DB	61	SGSSSGHTASLTITGAQAEDADYVCNSRDSSGNHVFEGGKTLTVLG	108		
RESULT 2					
HV3T_HUMAN					
ID	HV3T_HUMAN	STANDARD:	PRT:	116 AA.	
AC	P01781:				

```

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=75059123; PubMed=4803843;
RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT type), subgroup H III. Architecture of the complete IgM-molecule.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN [2]
RP REVISION 20-28-33.
RA Hilschmann N.;
RL Submitted (JUN-1975) to the PIR data bank.
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
CC PIR: A02064; M3HUGL.
DR HSSP: P01772; 2F84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match
Best Local Similarity 26.8%; Score 437.5; DB 1; Length 116;
Matches 84; Conservative 12; Mismatches 20; Indels 5; Gaps 1;

OY 40 EVQLVDSGGGVPRPGSLRLSCAASGFTTDDYGMKVRAPKGLKLEWVSGIMNGSTCY 99
    |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVQLVESGDLVQPGSLRLSCAASGFTFBBLGMVTRVAPKGLKLEWVNIKZBSGZBY 60
OY 100 ADSVGRVITISRDNAKNSLYLQMNSLRARDTAVYVYCAKLTIGAGRGVPFLMGKGTIVYS 159
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 VDSVGRFTISRDNAKNSLYLQMNSLRARDTAVYVYCAKLTIGAGRGVPLMGKGTIVYS 115
OY 160 S 160
DB 116 T 116

RESULT 3
ID HV3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region BDT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human

```

```

RT IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPIC, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02050; A2HUBU.
DR HSSP: P01789; 1MCP.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DE52DCF4 CRC64;

Query Match
Best Local Similarity 26.7%; Score 436; DB 1; Length 115;
Matches 85; Conservative 18; Mismatches 12; Indels 6; Gaps 2;

OY 40 EVQLVDSGGGVPRPGSLRLSCAASGFTTDDYGMKVRAPKGLKLEWVSGIMNGSTCY 99
    |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 EVQLVESGDLVQPGSLRLSCAASGFTVBSHSMVTRVAPKALZWSAI YRGGTYVY 59
OY 100 ADSVGRVITISRDNAKNSLYLQMNSLRARDTAVYVYCAKLTIGAGRGVPFLMGKGTIVYS 159
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 60 ADSVGRFTISRDNSRIVYLLQMSLRARDTAVYVYCAKLTIGAGRGVPLMGKGTIVYS 114
OY 160 S 160
DB 115 S 115

RESULT 4
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=81101090; PubMed=6450418;
RA Mathysens G., Rabbits T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00236; AA53516.1; -.
DR EMBL: M35415; AA58735.1; -.
DR PIR: A02047; H3H026.
DR PDB: 1HOU; 23-DEC-99.
DR Genbank: HGNC:5545; IGHV@.
DR GO: GO:0005576; C:extracellular; NAS.

```

```
DR GO:0003823; F:antigen binding activity; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-LIKE.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 26.3%; Score 429; DB 1; Length 117;
Best Local Similarity 82.7%; Pred. No. 2.6e-24;
Matches 81; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 40 EVQLVQSGGVERPGGSLRLSCAASGFTFDYGMQSVRQAPGKGLVWVSGINMGSGTGY 99
DB 20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVRQAPGKGLVWVAISGSGSTYY 79

QY 100 ADSVKGRTYISHDNAKNSLYLQMSLRAEDTAVYYCAK 137
DB 80 GDSVKGRTYISHDNSKNTLYLQMSLRAEDTAVYYCAK 117

RESULT 5
HV3J_HUMAN
ID HV3J_HUMAN STANDARD; PRT; 121 AA.
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region H1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;

CC -1- SIMILARITY: Contains 1 Immunoglobulin-like domain.
CC PIR: A02054; GIHHL.
DR HSSP: P01772; 2F84.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding activity; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-LIKE.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyroliidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 26.2%; Score 428; DB 1; Length 121;
Best Local Similarity 67.8%; Pred. No. 3.2e-24;
Matches 82; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

QY 40 EVQLVQSGGVERPGGSLRLSCAASGFTFDYGMQSVRQAPGKGLVWVSGINMGSGTGY 99
DB 61 EVQLVQSGGVERPGGSLRLSCAASGFTFDYGMQSVRQAPGKGLVWVSGINMGSGTGY 99
```

```
DB 1 QVKLVQAGGVVQPGGSLRLSCIASGFTFSNYGMHVRQAPGKGLVWVAIYNGSRTYY 60
QY 100 ADSVKGRTYISHDNAKNSLYLQMSLRAEDTAVYYCAKLTGARGVFPDLMGKGTYYVS 159
DB 61 GDSVKGRTYISHDNSKNTLYLQMSLRAEDTAVYYCAKPDILTAFSPDYGQGLVYVS 120

QY 160 S 160
DB 121 S 121

RESULT 6
HV3J_HUMAN
ID HV3J_HUMAN STANDARD; PRT; 120 AA.
AC P01782;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region DOB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;

CC -1- SIMILARITY: Contains 1 Immunoglobulin-like domain.
CC PIR: A90431; GIHDB.
DR HSSP: P01772; 2F84.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding activity; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-LIKE.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13440 MW; 880DDE307C4B2627 CRC64;

Query Match 26.0%; Score 424.5; DB 1; Length 120;
Best Local Similarity 67.7%; Pred. No. 5.6e-24;
Matches 84; Conservative 10; Mismatches 23; Indels 7; Gaps 2;

QY 40 EVQLVQSGGVERPGGSLRLSCAASGFTFDYGMQSVRQAPGKGLVWVSGINMGSGTGY 99
DB 1 EVQLVESGGDLVQPGGSLRLSCAASGFTNFHEYMHWLRGPKGPEWSTIWMNGSVLY 60

QY 100 ADSVKGRTYISHDNAKNSLYLQMSLRAEDTAVYYCAKLTGARGV--YFDLMGKGTYY 156
DB 61 ADSVKGRTYISHDNAKNTLYLQNLTRPEDTAVYYCAK---GYLMNGMWFDSMGQGLTY 116

QY 157 TVSS 160
DB 117 TVSS 120
```



```

DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 108 IG-LIKE.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match 25.7%; Score 419; DB 1; Length 115;
Best Local Similarity 68.6%; Pred. No. 1.3e-23;
Matches 83; Conservative 12; Mismatches 20; Indels 6; Gaps 2;

OY 40 EVOLVSGGVERPGSLRLSCAASGFTDDYGMHWQAQPGKGLEWVSGINMNGSTGY 99
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYVMSWRQAQCKGLZVGAALZGLSVSZSY 60

OY 100 ADVSKGRVITSRDNKNSLYLQNMNSLRADPTAVYYCAKILGAGRWYFDLNGKGTYYVS 159
DB 61 ADVSKGRFTISRDKSKNT---MNSLRADPTAVYYCAK--GKVSAYYFBYWGZGLTVTVS 114

OY 160 S 160
DB 115 S 115

RESULT 10
HV31_HUMAN STANDARD; PRT; 119 AA.
AC P01770;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-IIr region NIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE-77070269; PubMed-826475;
RA Ponslingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
RT monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The
RT chymotryptic peptides of the H-chain, alignment of the tryptic
RT peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE-77070267; PubMed-1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nle). I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanoogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG1 MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A9168; G1HUNT.
DR HSSP: P01772; 2PB4.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Pyroliidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYROLIIDONE CARBOXYLIC ACID.

```

```

FT DISULFID 22 96
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13242 MW; C96935A6E55E165B CRC64;

Query Match 25.3%; Score 413; DB 1; Length 119;
Best Local Similarity 66.9%; Pred. No. 3.7e-23;
Matches 81; Conservative 15; Mismatches 23; Indels 2; Gaps 1;

OY 40 EVOLVSGGVERPGSLRLSCAASGFTDDYGMHWQAQPGKGLEWVSGINMNGSTGY 99
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSRTTHWQAQPGKGLEWVAVMSYGBBKHV 60

OY 100 ADVSKGRVITSRDNKNSLYLQNMNSLRADPTAVYYCAKILGAGRWYFDLNGKGTYYVS 159
DB 61 ADVSKGRFTISRDNKNSLYLQNMNSLRADPTAVYYCAK--RDPAFPAHNGGTLTVVS 118

OY 160 S 160
DB 119 S 119

RESULT 11
HV01_CANFA STANDARD; PRT; 114 AA.
AC P01784;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region GOM.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE-77242268; PubMed-407924;
RA Wasserman R.L., Capra J.D.;
RT "Primary structure of the variable regions of two canine
RT immunoglobulin heavy chains.";
RL Biochemistry 16:3160-3168(1977).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02067; AYDGM.
DR HSSP: P01772; 2PB4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12430 MW; BID745D2C4E13C4 CRC64;

Query Match 25.3%; Score 412.5; DB 1; Length 114;
Best Local Similarity 67.8%; Pred. No. 3.8e-23;
Matches 82; Conservative 11; Mismatches 21; Indels 7; Gaps 1;

OY 40 EVOLVSGGVERPGSLRLSCAASGFTDDYGMHWQAQPGKGLEWVSGINMNGSTGY 99
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYDQWVAQAPGKGLQVAFNDALSAQY 60

OY 100 ADVSKGRVITSRDNKNSLYLQNMNSLRADPTAVYYCAKILGAGRWYFDLNGKGTYYVS 159
DB 61 ADAVSKGRFTISRDNKNSLYLQNMNSLRADPTAVYYCAK-----WQFEYWGSGTLTVVS 113

OY 160 S 160
DB 114 S 114

RESULT 12

```



```

QY 40 EVQIVQSGGGERPGSLRLSCASGFTFDDYGMMSVROAPGKLGLEWVSGIMNNGSTGY 99
    1 QVZLVZSGGAVZPGRSLRLSCASGFSFTYAMHWROAPGKGLZMLSVISYBGBZYY 60
DB 100 ADVSVKGRVTISRDNKNSLYLQMNSLRAEDTAVYYCAK---ILGARGHYFDLMKGTIV 156
    61 AASVKGRTTISRBSBRTMYLEMSLRAENTAVVYCAKSGIALGSAVAG--TDYWGZGTLY 118
QY 157 TVSS 160
    119 TISS 122
DB

RESULT 15
HY20_MOUSE
ID HY20_MOUSE STANDARD: PRT: 122-AA.
AC P01789;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 19 heavy chain V region M603.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80199926; PubMed=6769593;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
RT three segments of DNA: VH, D and JH."
RL Cell 19:981-992(1980).
RN [2]
RP SEQUENCE OF 1-120.
RX MEDLINE=75017346; PubMed=4213527;
RA Rudikoff S., Potter M.;
RT "Variable region sequence of the heavy chain from a phosphorylcholine
RT binding myeloma protein."
RL Biochemistry 13:4033-4038(1974).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF FAB FRAGMENT.
RX MEDLINE=75065510; PubMed=4530984;
RA Segal D.M., Padlan E.A., Cohen G.H., Rudikoff S., Potter M.,
RA Davies D.R.;
RT "The three-dimensional structure of a phosphorylcholine-binding mouse
RT immunoglobulin Fab and the nature of the antigen binding site."
RL Proc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: B90795; AVMS63.
DR PDB: 1MCP; 15-JUL-92.
DR PDB: 2MCP; 15-JUL-92.
DR InterPro: IPR007110; 19-1-like.
DR InterPro: IPR003006; 19_MHC.
DR InterPro: IPR003596; 19_V.
DR Pfam: PF00047; 1g: 1.
DR SMART: SM00406; 1g: 1.
DR PROSITE: PS50835; 1g_LIKE; 1.
DR Immunoglobulin V region; 3D-structure.
FT DOMAIN 1 121
FT SITE 33 33
FT SITE 33 33
FT SITE 52 52
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 17 25
FT TURN 30 31
FT STRAND 33 39
FT TURN 41 42
FT STRAND 46 50

```

```

FT TURN 54 55
FT STRAND 61 61
FT TURN 64 69
FT STRAND 70 75
FT TURN 76 79
FT STRAND 80 86
FT HELIX 90 92
FT STRAND 94 103
FT STRAND 107 112
FT STRAND 116 120
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13626 MW; BA2C864438B64F0F CRC64;

Query Match 24.8%; Score 404.5; DB 1; Length 122;
Best Local Similarity 63.4%; Pred. No. 1.5e-22;
Matches 78; Conservative 17; Mismatches 25; Indels 3; Gaps 2;

QY 40 EVQIVQSGGGERPGSLRLSCASGFTFDDYGMMSVROAPGKLGLEWVSGIMNNG--ST 97
    1 EVKLIVSGGGLVQPGSLRLSCATSGFTFSDYMEMVROPPGKRLLEWIAASRNKNGKYYT 60
DB 98 GYADSVKGRVTISRDNKNSLYLQMNSLRAEDTAVYYCAKILGARGHYFDLMKGTIV 157
    1 EYSASVKGRTTISRBSBRTMYLEMSLRAENTAVVYCAKRY-YGSTWYFDWAGAGTIV 119
QY 158 VSS 160
    119 TISS 122
DB

```

Search completed: September 22, 2003, 15:13:48
Job time : 12.6165 secs

QY 1 MTMTIPPSFGAEFLLEIFNVKLLFAIPLVPPFYAAQPMAAEVQLVQSGGGYERPGGSLRLS 60
|||||
1 MTMTIPPSFGAEFLLEIFNVKLLFAIPLVPPFYAAQPMAAEVQLVQSGGGYERPGGSLRLS 60
Db 1 MTMTIPPSFGAEFLLEIFNVKLLFAIPLVPPFYAAQPMAAEVQLVQSGGGYERPGGSLRLS 60

RC TISSUE-Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013656; AAH13656.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 52.2793 Seconds
(without alignments)
947.272 Million cell updates/sec

Title: US-10-052-798-10
Perfect score: 1642
Sequence: 1 MTMTSPSGAFLEIFNVKK.....HHGAAERKLSEEDLNGAA 312

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_19Jun03:.*
1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1642	100.0	312	20	AAW83323
2	1642	100.0	312	23	ABB09604
3	1642	100.0	312	24	ABG74385
4	1460.5	88.9	309	20	AAW83322
5	1460.5	88.9	309	23	ABB09603
6	1460.5	88.9	309	24	ABG74384
7	1231	75.0	310	20	AAW83324
8	1231	75.0	310	23	ABB09605
9	1231	75.0	310	24	ABG74386

10	1194	72.7	277	23	ABG91841	Human antibody fire
11	1194	72.7	277	23	ABG92019	Human antibody fire
12	1194	72.7	277	23	ABG78150	Human Fv molecule
13	1194	72.7	277	23	ABG78328	Human Fv molecule
14	1192	72.6	247	23	ABP45459	Human Blys binding
15	1188	72.4	263	23	ABG92024	Antibody protein #
16	1178.5	71.8	260	23	ABG92023	Antibody protein #
17	1176.5	71.7	282	22	AAE02185	PAM1 single chain
18	1162	70.8	251	23	ABP45583	Human Blys binding
19	1149	70.0	249	23	ABP45098	Human Blys binding
20	1149	70.0	251	23	ABP44941	Human Blys binding
21	1142	69.5	251	23	ABP44971	Human Blys binding
22	1141.5	69.5	266	23	ABG92020	Human antibody fire
23	1139.5	69.4	256	23	ABP45178	Human Blys binding
24	1138.5	69.3	248	23	ABP44905	Human Blys binding
25	1134.5	69.1	248	23	ABP44903	Human Blys binding
26	1134	69.1	237	23	ABP46101	Human Blys binding
27	1133.5	69.0	248	23	ABP44824	Human Blys binding
28	1133	69.0	237	23	ABP46028	Human Blys binding
29	1133	69.0	247	23	ABP44913	Human Blys binding
30	1132.5	69.0	248	23	ABP45312	Human Blys binding
31	1132.5	69.0	290	24	ABP55318	pelb/5AR/twrc/6his
32	1127	68.6	247	23	ABP45753	Human Blys binding
33	1125.5	68.5	240	23	ABP45901	Human Blys binding
34	1125.5	68.5	296	23	ABG60637	Immunoglobulin rel
35	1125	68.5	237	23	ABP45995	Human Blys binding
36	1125	68.5	249	23	ABP45713	Human Blys binding
37	1124.5	68.5	252	23	ABP45720	Human Blys binding
38	1124	68.5	243	23	ABP46045	Human Blys binding
39	1123.5	68.4	240	23	ABP46002	Human Blys binding
40	1123.5	68.4	248	23	ABP44902	Human Blys binding
41	1122	68.3	239	23	ABP46024	Human Blys binding
42	1122	68.3	249	23	ABP45714	Human Blys binding
43	1122	68.3	291	23	AAE92022	Single chain antib
44	1120	68.2	291	23	ABG60632	Immunoglobulin rel
45	1119	68.1	239	23	ABP46007	Human Blys binding

ALIGNMENTS

RESULT 1	
AAW83323	standard; Protein: 312 AA.
AAW83323;	
16-MAR-1999	(first entry)
Single chain Apo-2 antibody 2066.	
Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer; tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;	
TNF cytokine.	
xx	
OS	Homo sapiens.
xx	
PN	W09851793-A1.
xx	
PD	19-NOV-1998.
xx	
PF	14-MAY-1998; 98WO-US09704.
xx	
PR	09-FEB-1998; 98US-0020746.
xx	
PR	15-MAY-1997; 97US-0857216.
xx	
PA	(GETH) GENENTECH INC.
xx	
PI	Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
xx	WPI; 1999-045228/04.
DR	N-PSDB; AAV72533.
xx	

Human Apo-2 polypeptide inducing apoptosis - useful to treat conditions linked with decreased apoptosis e.g. cancer, and produce antibodies to increase or decrease apoptosis

Example 14; Fig 16; 134pp; English.

The present invention describes human Apo-2. Apo-2 can be used therapeutically to induce apoptosis in mammalian cells, and so is useful to treat conditions associated with decreased apoptosis e.g. cancer. Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It can be used to identify agents activating Apo-2, useful to treat mammalian cancer cells, and to produce Apo-2 chimeras useful therapeutically (e.g. those containing immunoglobulin sequences can be inhibit apoptosis) or diagnostically (e.g. those comprising an epitope tag polypeptide allow Apo-2 detection and purification using anti-tag antibodies). It can be used to produce antibodies which can be combined with a (particularly pharmaceutically acceptable) carrier in compositions or used to produce dimeric molecules (especially homodimeric molecules comprising first and second Apo-2 antibodies). Agonistic (especially single-chain) antibodies can be administered to induce apoptosis in mammalian cancer cells, and antagonistic antibodies used to block excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2 antibodies may also be used diagnostically e.g. to detect Apo-2 expression in cells/tissues and in Apo-2 purification. The present sequence represents a single chain Apo-2 antibody, designated 20E6.

Sequence 312 AA:

Query Match 100.0%; Score 1642; DB 20; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.6e-101;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTMTSPSGAFLEIFNVKLLFAIPLVVPPYAAQAPAMAGVOLVESGGGLVOPGSLRLS 60
DB 1 MTMTSPSGAFLEIFNVKLLFAIPLVVPPYAAQAPAMAGVOLVESGGGLVOPGSLRLS 60
QY 61 CAASGFTSSYWMVSWRQAPGKLEWVANIKODSEKYYVDSYVKGRFTISRDNKNSLYL 120
DB 61 CAASGFTSSYWMVSWRQAPGKLEWVANIKODSEKYYVDSYVKGRFTISRDNKNSLYL 120
QY 121 OMNSLRADPTAVVYCARDLKVKSSSGMFPDWGKGTIVTVSSGGGSGGGSGGSSSE 180
DB 121 OMNSLRADPTAVVYCARDLKVKSSSGMFPDWGKGTIVTVSSGGGSGGGSGGSSSE 180
QY 181 LTQDPAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLYTGKNNRPSGIPDRFSG 240
DB 181 LTQDPAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLYTGKNNRPSGIPDRFSG 240
QY 241 SSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGKTLVLGAANHHNHHGADEQ 300
DB 241 SSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGKTLVLGAANHHNHHGADEQ 300
QY 301 KLISEEDLNGAA 312
DB 301 KLISEEDLNGAA 312

RESULT 2
ABBO9604
ID ABB09604 standard; Protein; 312 AA.

AC ABB09604;

DT 29-MAY-2002 (first entry)

DE Amino acid sequence of single-chain Apo-2 antibody 20E6.

KW Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;

KW caspase; apoptosis; cancer; antibody.

OS Bacteriophage.

XX US6342369-B1.
PN 29-JAN-2002.

XX 14-MAY-1998; 98US-0079029.

XX 15-MAY-1997; 97US-046615P.

XX 09-FEB-1998; 98US-074119P.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ;

XX WPI; 2002-224941/28.

XX N-PSDB; AB41734.

XX New nucleic acids encoding an Apo-2 ligand, useful for activating or stimulating apoptosis in cancer cells, thus especially useful in the treatment of cancer, or in enhancing immune-mediated cell death -

XX Example 14; Fig 16; 68pp; English..

The present sequence represents a single-chain Apo-2 antibody, designated 20E6, which is isolated from a phage library. It is believed that Apo-2 is a member of the tumour necrosis factor receptor (TNFR) family. Apo-2 polypeptide is capable of triggering caspase-dependent apoptosis and activating nuclear factor-kappa B, a soluble extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2 antibodies may be used to activate or stimulate apoptosis in cancer cells. They are therefore especially useful in the treatment of cancer, to enhance immune-mediated cell death in cells expressing Apo-2, to detect expression of Apo-2 in specific cells, tissues or serum, and in affinity purification of Apo-2 from recombinant cell culture or natural sources.

Sequence 312 AA:

Query Match 100.0%; Score 1642; DB 23; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.6e-101;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTMTSPSGAFLEIFNVKLLFAIPLVVPPYAAQAPAMAGVOLVESGGGLVOPGSLRLS 60
DB 1 MTMTSPSGAFLEIFNVKLLFAIPLVVPPYAAQAPAMAGVOLVESGGGLVOPGSLRLS 60
QY 61 CAASGFTSSYWMVSWRQAPGKLEWVANIKODSEKYYVDSYVKGRFTISRDNKNSLYL 120
DB 61 CAASGFTSSYWMVSWRQAPGKLEWVANIKODSEKYYVDSYVKGRFTISRDNKNSLYL 120
QY 121 OMNSLRADPTAVVYCARDLKVKSSSGMFPDWGKGTIVTVSSGGGSGGGSGGSSSE 180
DB 121 OMNSLRADPTAVVYCARDLKVKSSSGMFPDWGKGTIVTVSSGGGSGGGSGGSSSE 180
QY 181 LTQDPAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLYTGKNNRPSGIPDRFSG 240
DB 181 LTQDPAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLYTGKNNRPSGIPDRFSG 240
QY 241 SSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGKTLVLGAANHHNHHGADEQ 300
DB 241 SSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGKTLVLGAANHHNHHGADEQ 300
QY 301 KLISEEDLNGAA 312
DB 301 KLISEEDLNGAA 312

RESULT 3
ABG74385
ID ABG74385 standard; Protein; 312 AA.

AC ABG74385;

XX

DT 11-APR-2003 (first entry)
XX Single chain antibody (scFv) fragment 20E6.
DE
XX
XX Apo-2; tumour necrosis factor family: TNFR; gene therapy;
KW apoptosis; tissue-specific typing; affinity purification;
KW competitive-type receptor binding assay; mouse; 20E6.
XX
XX Mus sp.
OS
XX
XX US2002150985-A1.
PN
XX
XX 17-OCT-2002.
PD
XX
XX 02-NOV-2001; 2001US-0052798.
PF
XX
XX 15-MAY-1997; 97US-046615P.
PR 09-FEB-1998; 98US-074113P.
PR 14-MAY-1998; 98US-0079029.
XX
XX (GETH) GENENTECH INC.
PA
XX
XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
PI WPI; 2003-198287/19.
XX
XX N-PSDB; ABX16408.
DR
XX
XX New Apo-2 polypeptides and polynucleotides, useful for inducing
PT apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in
PT quantitative diagnostic assays, or in generating antibodies against
PT Apo-2 -
XX
XX
XX Example 14; Fig 16; 64pp; English.
PS
XX
XX The invention describes a novel isolated Apo-2 polypeptide. The Apo-2
CC polypeptide is useful for inducing apoptosis in mammalian cells, in vivo
CC or ex vivo gene therapy, in quantitative diagnostic assays, as a control
CC against samples containing unknown quantities of Apo-2, in generating
CC antibodies, in affinity purification techniques, and in competitive-type
CC receptor binding assays when labelled with, for instance, radioiodine,
CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a
CC diagnostic for tissue-specific typing. This is the amino acid sequence
CC of the single chain antibody fragment (scFv) 20E6 used in the
CC preparation of anti-apo-2 antibodies.
CC
XX
XX Sequence 312 AA:
SQ
Query Match 100.0%; Score 1642; DB 24; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.6e-101;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MTMTTPEFGAFLEIFNVKKLLFAIRLVVPFYAAQPMAGVOLVESGGGLVPGSGRLS 60
DB 1 MTMTTPEFGAFLEIFNVKKLLFAIRLVVPFYAAQPMAGVOLVESGGGLVPGSGRLS 60
OY 61 CAASGFTSSYMWMSWVQADPKGLKLEWVANIKODSEKRYVDSYKGRFTISRDNKNSLYL 120
DB 61 CAASGFTSSYMWMSWVQADPKGLKLEWVANIKODSEKRYVDSYKGRFTISRDNKNSLYL 120
OY 121 QMNSLRADRYAVYYCARNLLKVGSSSGWFDPMGRGTTVVSSGGGSGGSGGSSSE 180
DB 121 QMNSLRADRYAVYYCARNLLKVGSSSGWFDPMGRGTTVVSSGGGSGGSGGSSSE 180
OY 181 LTQDDPAVSVALGQTVRTTCGDSLSRYASWYQOQKPGQAVLVLYGKNNRPSGIPDRFSG 240
DB 181 LTQDDPAVSVALGQTVRTTCGDSLSRYASWYQOQKPGQAVLVLYGKNNRPSGIPDRFSG 240
OY 241 SSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFEGGKTLTYLGAANHHHHHGADEQ 300
DB 241 SSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFEGGKTLTYLGAANHHHHHGADEQ 300
OY 301 KLISEEDLNGAA 312
|||||

DB 301 KLISEEDLNGAA 312
RESULT 4
ID AAW83322
AAW83322 standard; Protein; 309 AA.
AC
XX AAW83322;
XX
XX 16-MAR-1999 (first entry)
DE Single chain Apo-2 antibody 16E2.
XX
XX Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
KW TNF cytokine.
XX
XX Homo sapiens.
OS
XX WO9851793-A1.
PN
XX
XX 19-NOV-1998.
PD
XX
XX 14-MAY-1998; 98WO-US09704.
PF
XX
XX 09-FEB-1998; 98US-0020746.
PR 15-MAY-1997; 97US-0857216.
XX
XX (GETH) GENENTECH INC.
PA
XX
XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
PI WPI; 1999-045228/04.
XX
XX N-PSDB; AAV72532.
DR
XX
XX Human Apo-2 polypeptide inducing apoptosis - useful to treat
PT conditions linked with decreased apoptosis e.g. cancer, and produce
PT antibodies to increase or decrease apoptosis
XX
XX
XX Example 14; Fig 16; 134pp; English.
PS
XX
XX The present invention describes human Apo-2. Apo-2 can be used
CC therapeutically to induce apoptosis in mammalian cells, and so is useful
CC to treat conditions associated with decreased apoptosis e.g. cancer.
CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor
CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by
CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It
CC can be used to identify agents activating Apo-2, useful to treat
CC mammalian cancer cells, and to produce Apo-2 chimeras useful
CC therapeutically (e.g. those containing immunoglobulin sequences can be
CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
CC tag polypeptide allow Apo-2 detection and purification using anti-tag
CC antibodies). It can be used to produce antibodies which can be combined
CC with a (particularly pharmaceutically acceptable) carrier in compositions
CC or used to produce dimeric molecules (especially homodimeric molecules
CC comprising first and second Apo-2 antibodies). A agonistic (especially
CC single-chain) antibodies can be administered to induce apoptosis in
CC mammalian cancer cells, and antagonistic antibodies used to block
CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
CC antibodies may also be used diagnostically e.g. to detect Apo-2
CC expression in cells/tissues and in Apo-2 purification. The present
CC sequence represents a single chain Apo-2 antibody, designated 16E2.
XX
SQ
Sequence 309 AA:
Query Match 88.9%; Score 1460.5; DB 20; Length 309;
Best Local Similarity 90.1%; Pred. No. 1.9e-89;
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;
OY 1 MTMTTPEFGAFLEIFNVKKLLFAIRLVVPFYAAQPMAGVOLVESGGGLVPGSGRLS 60
DB 1 MTMTTPEFGAFLEIFNVKKLLFAIRLVVPFYAAQPMAGVOLVESGGGLVPGSGRLS 60
|||||

QY 61 CAASGFTSSYWMVNRQAPGKLEWVANIKODGSEKTYVDSVKGRFTISRDNKNSLYL 120
 ||||| : : : : :
 Db 61 CAASGFTDDYGMVNRQAPGKLEWVSGIMNNGSTGYADSVKGRVYISRDNKNSLYL 120
 QY 121 QMNSLRADTAVYTCARDLKLVKSGSSGW-FDPMCRGTTVYVSSGGSGGGSGGSS 179
 ||||| : : : : :
 Db 121 QMNSLRADTAVYTCARDLKLVKSGSSGW-FDPMCRGTTVYVSSGGSGGGSGGSS 176
 ||||| : : : : :
 QY 180 ELTODPAVSVALGQVTRITTCOGDSLRSYASWYQOKPCQAPVLYVYGNRPSCGIPDRFS 239
 ||||| : : : : :
 Db 177 ELTODPAVSVALGQVTRITTCOGDSLRSYASWYQOKPCQAPVLYVYGNRPSCGIPDRFS 236
 ||||| : : : : :
 QY 240 GSSSGNTASLTITGAQADEADYYCNSRDSSGNHVFEGGTRKLYLGAHHHHHGAEE 299
 ||||| : : : : :
 Db 237 GSSSGNTASLTITGAQADEADYYCNSRDSSGNHVFEGGTRKLYLGAHHHHHGAEE 296
 ||||| : : : : :
 QY 300 OKLISEEDLNGAA 312
 ||||| : : : : :
 Db 297 OKLISEEDLNGAA 309

RESULT 5
 ID ABB09603
 ABB09603 standard; Protein; 309 AA.

AC ABB09603;
 XX
 DT 29-MAY-2002 (first entry)

DE Amino acid sequence of single-chain Apo-2 antibody 16E2.

KM Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;
 KW caspase; apoptosis; cancer; antibody.

OS Bacteriophage.

PN US6342369-B1.

PD 29-JAN-2002.

PF 14-MAY-1998; 98US-0079029.

PR 15-MAY-1997; 97US-046615P.

PR 09-FEB-1998; 98US-074119P.

PA (GETH) GENENTECH INC.

PI Ashkenazi AJ;

DR WPI: 2002-224941/28.

DR N-PSDB; ABL41733.

PT New nucleic acids encoding an Apo-2 ligand, useful for activating or
 stimulating apoptosis in cancer cells, thus especially useful in the
 treatment of cancer, or in enhancing immune-mediated cell death
 XX
 PS Example 14; Fig 16; 68pp; English.

CC The present sequence represents a single-chain Apo-2 antibody, designated
 CC 16E2, which is isolated from a phage library. It is believed that
 CC Apo-2 is a member of the tumour necrosis factor receptor (TNFR)
 CC family. Apo-2 polypeptide is capable of triggering caspase-dependent
 CC apoptosis and activating nuclear factor-kappa B. A soluble
 CC extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2
 CC antibodies may be used to activate or stimulate apoptosis in cancer
 CC cells. They are therefore especially useful in the treatment of cancer,
 CC to enhance immune-mediated cell death in cells expressing Apo-2, to
 CC detect expression of Apo-2 in specific cells, tissues or serum, and in
 CC affinity purification of Apo-2 from recombinant cell culture or natural
 CC sources.

XX Sequence 309 AA;

Query Match 88.9%; Score 1460.5; DB 23; Length 309;
 Best Local Similarity 90.1%; Pred. No. 1.9e-89;
 Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;

QY 1 MTMTIPSGAFLEIFENYKILFALPIVPPYAQAQPAAGVQVDSGGGLVQPGSLRLS 60
 ||||| : : : : :
 Db 1 MTMTIPSGAFLEIFENYKILFALPIVPPYAQAQPAAGVQVDSGGGLVQPGSLRLS 60
 ||||| : : : : :
 QY 61 CAASGFTSSYWMVNRQAPGKLEWVANIKODGSEKTYVDSVKGRFTISRDNKNSLYL 120
 ||||| : : : : :
 Db 61 CAASGFTDDYGMVNRQAPGKLEWVSGIMNNGSTGYADSVKGRVYISRDNKNSLYL 120
 ||||| : : : : :
 QY 121 QMNSLRADTAVYTCARDLKLVKSGSSGW-FDPMCRGTTVYVSSGGSGGGSGGSS 179
 ||||| : : : : :
 Db 121 QMNSLRADTAVYTCARDLKLVKSGSSGW-FDPMCRGTTVYVSSGGSGGGSGGSS 176
 ||||| : : : : :
 QY 180 ELTODPAVSVALGQVTRITTCOGDSLRSYASWYQOKPCQAPVLYVYGNRPSCGIPDRFS 239
 ||||| : : : : :
 Db 177 ELTODPAVSVALGQVTRITTCOGDSLRSYASWYQOKPCQAPVLYVYGNRPSCGIPDRFS 236
 ||||| : : : : :
 QY 240 GSSSGNTASLTITGAQADEADYYCNSRDSSGNHVFEGGTRKLYLGAHHHHHGAEE 299
 ||||| : : : : :
 Db 237 GSSSGNTASLTITGAQADEADYYCNSRDSSGNHVFEGGTRKLYLGAHHHHHGAEE 296
 ||||| : : : : :
 QY 300 OKLISEEDLNGAA 312
 ||||| : : : : :
 Db 297 OKLISEEDLNGAA 309

RESULT 6
 ID ABG74384
 ABG74384 standard; Protein; 309 AA.

AC ABG74384;

DT 11-APR-2003 (first entry)

DE Single chain antibody (scFv) fragment 16E2.

KM Apo-2; tumour necrosis factor family; TNFR; gene therapy;
 KW apoptosis; tissue-specific typing; affinity purification;
 KW competitive-type receptor binding assay; mouse; 16E2.

OS Mus sp.

PN US2002150985-A1.

PD 17-OCT-2002.

PF 02-NOV-2001; 2001US-0052798.

PR 15-MAY-1997; 97US-046615P.

PR 09-FEB-1998; 98US-074119P.

PR 14-MAY-1998; 98US-0079029.

PA (GETH) GENENTECH INC.

PI Adams CW, Ashkenazi AJ, Chuntharapal A, Kim KJ;

DR WPI: 2003-198287/19.

DR N-PSDB; ABX16407.

PT New Apo-2 polypeptides and polynucleotides, useful for inducing
 apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in
 PT quantitative diagnostic assays, or in generating antibodies against
 Apo-2
 XX
 PS Example 14; Fig 16; 64pp; English.

CC The invention describes a novel isolated Apo-2 polypeptide. The Apo-2
 CC polypeptide is useful for inducing apoptosis in mammalian cells, in vivo
 CC or ex vivo gene therapy, in quantitative diagnostic assays, as a control
 CC against samples containing unknown quantities of Apo-2, in generating

CC antibodies, in affinity purification techniques, and in competitive-type
 CC receptor binding assays when labelled with, for instance, radiolodine,
 CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a
 CC diagnostic for tissue-specific typing. This is the amino acid sequence
 CC of the single chain antibody fragment (scFv) 16E2 used in the
 CC preparation of anti-apo-2 antibodies.

XX Sequence 309 AA;

Query Match 88.9%; Score 1460.5; DB 24; Length 309;
 Best Local Similarity 90.1%; Pred. No. 1.9e-89;
 Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;

QY 1 MTMTTPSGAFLEIFNVKKLLFAIPLVPEFYAOPAMAGVOLVESGGGLVPGSGRLS 60
 DB 1 MTMTTPSGAFLEIFNVKKLLFAIPLVPEFYAOPAMAEQVLQVSGGVERPGSGRLS 60
 QY 61 CAASGFTFFSYWMSVWQAPKGLKLEWVANIKODGSEKYYDVSVKGRFTISRDNKNSLYL 120
 DB 61 CAASGFTFFDYGMWVWQAPKGLKLEWVSGIWMNGSGTYADSVKGRVYISRDNKNSLYL 120
 QY 121 QMNSLRADPFAVYYCARDLKVKGSSSGW-FDPWGRGTYYVSSGGSGSGSGSGSGSS 179
 DB 121 QMNSLRADPFAVYYCA---KILGAGRWTFDLWGKGTYYVSSGGSGSGSGSGSGSS 176
 QY 180 ELTODPAVSVALGQTVRITCGDSLRSYASWYQOKPGQAPVLVIYKNNRPSGIPRFS 239
 DB 177 ELTODPAVSVALGQTVRITCGDSLRSYASWYQOKPGQAPVLVIYKNNRPSGIPRFS 236
 QY 240 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGSGTKLTVLGAHHHHHGAEE 299
 DB 237 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGSGTKLTVLGAHHHHHGAEE 296
 QY 300 OKLISEEDLNGAA 312
 DB 297 OKLISEEDLNGAA 309

RESULT 7

AAW83324 ID AAW83324 standard; Protein: 310 AA.

AC AAW83324;

XX 16-MAR-1999 (first entry)

XX Single chain Apo-2 antibody 24C4.

XX Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
 KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
 XX TNF cytokine.

XX Homo sapiens.

XX MO9851793-A1.

XX 19-NOV-1998.

XX 14-MAY-1998; 98WO-US09704.

XX 09-FEB-1998; 98US-0020746.

XX 15-MAY-1997; 97US-0857216.

XX (GERTH) GENENTECH INC.

XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KU;

XX WPI; 1999-045228/04.

XX N-PSDB: AAV72534.

XX Human Apo-2 polypeptide inducing apoptosis - useful to treat
 PT conditions linked with decreased apoptosis e.g. cancer, and produce
 PT antibodies to increase or decrease apoptosis

XX Example 14; Fig 16; 134pp: English.

XX The present invention describes human Apo-2. Apo-2 can be used
 PS therapeutically to induce apoptosis in mammalian cells, and so is useful
 CC to treat conditions associated with decreased apoptosis e.g. cancer.
 CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor
 CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by
 CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It
 CC can be used to identify agents activating Apo-2, useful to treat
 CC mammalian cancer cells, and to produce Apo-2 chimeras useful
 CC therapeutically (e.g. those containing immunoglobulin sequences can be
 CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
 CC tag polypeptide allow Apo-2 detection and purification using anti-tag
 CC antibodies). It can be used to produce antibodies which can be combined
 CC with a (particularly pharmaceutically acceptable) carrier in compositions
 CC or used to produce dimeric molecules (especially homodimeric molecules
 CC comprising first and second Apo-2 antibodies). Agonistic (especially
 CC single-chain) antibodies can be administered to induce apoptosis in
 CC mammalian cancer cells, and antagonistic antibodies used to block
 CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
 CC antibodies may also be used diagnostically e.g. to detect Apo-2
 CC expression in cells/tissues and in Apo-2 purification. The present
 CC sequence represents a single chain Apo-2 antibody, designated 24C4.

XX Sequence 310 AA;

Query Match 75.0%; Score 1231; DB 20; Length 310;
 Best Local Similarity 77.7%; Pred. No. 3.3e-74;
 Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;

QY 1 MTMTTPSGAFLEIFNVKKLLFAIPLVPEFYAOPAMAGVOLVESGGGLVPGSGRLS 60
 DB 1 MTMTTPSGAFLEIFNVKKLLFAIPLVPEFYAOPAMAEQVLQVSGGVERPGSGRLS 60
 QY 61 CAASGFTFFSYWMSVWQAPKGLKLEWVANIKODGSEKYYDVSVKGRFTISRDNKNSLYL 120
 DB 61 CAASGFTFFSYGMWVWQAPKGLKLEWVAGIFRYDGNKYUADSVKGRFTISRDNKNSLYL 120
 QY 121 QMNSLRADPFAVYYCARDLKVKGSSSGW-FDPWGRGTYYVSSGGSGSGSGSGSGSS 178
 DB 121 QMNSLRADPFAVYYCARDLKVKGSSSGW-FDPWGRGTYYVSSGGSGSGSGSGSGSS 172
 QY 179 -SELTODPAVSVALGQTVRITCGDSLRSYASWYQOKPGQAPVLVIYKNNRPSGIPRFS 234
 DB 173 QSVLTODPVSVALGQTVRITCGDSLRSYASWYQOKPGQAPVLVIYKNNRPSGIPRFS 232
 QY 235 PDRESGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGSGTKLTVLGAHHHHH 294
 DB 233 PDRESGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGSGTKLTVLGAHHHHH 292
 QY 295 HGAAEOKLISEEDLNGAA 312
 DB 293 HGAAEOKLISEEDLNGAA 310

RESULT 8

ABB09605 ID ABB09605 standard; Protein: 310 AA.

XX ABB09605;

XX 29-MAY-2002 (first entry)

XX Amino acid sequence of single-chain Apo-2 antibody 24C4.

XX Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;
 KW caspase; apoptosis; cancer; antibody.

XX Bacteriophage.

XX US6342369-B1.


```

PD 29-JAN-2002.
XX
XX 14-MAY-1998; 98US-0079029.
XX
XX 15-MAY-1997; 97US-046615P.
XX
XX 09-FEB-1998; 98US-074119P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ;
XX
XX WPI: 2002-224941/28.
XX
XX N-PSDB; ABL41735.
XX
XX New nucleic acids encoding an Apo-2 ligand, useful for activating or
XX stimulating apoptosis in cancer cells, thus especially useful in the
XX treatment of cancer, or in enhancing immune-mediated cell death
XX
XX Example 14; Fig 16; 68pp; English.
XX
XX The present sequence represents a single-chain Apo-2 antibody, designated
XX 24C4, which is isolated from a phage library. It is believed that
XX Apo-2 is a member of the tumour necrosis factor receptor (TNFR)
XX family. Apo-2 polypeptide is capable of triggering caspase-dependent
XX apoptosis and activating nuclear factor-kappa B. A soluble
XX extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2
XX antibodies may be used to activate or stimulate apoptosis in cancer
XX cells. They are therefore especially useful in the treatment of cancer,
XX to enhance immune-mediated cell death in cells expressing Apo-2, to
XX detect expression of Apo-2 in specific cells, tissues or serum, and in
XX affinity purification of Apo-2 from recombinant cell culture or natural
XX sources.
XX
XX Sequence 310 AA;
XX
XX Query Match 75.0%; Score 1231; DB 23; Length 310;
XX Best Local Similarity 77.7%; Pred. No. 3.3e-74;
XX Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;
XX
XX 1 MTMTSPSGAFLEIFNVKLLFAIPLVPPFYAAPAMAGVOLVSSGGGLVOPGSLRLS 60
XX 1 MTMTSPSGAFLEIFNVKLLFAIPLVPPFYAAPAMAGVOLVSSGGGLVOPGSLRLS 60
XX
XX 61 CAASGFTSSYWMVSWROAPKGLKLEWVANIKODSEKTYVSVKGRFTISRDNANSLYL 120
XX 61 CAASGFTSSYWMVSWROAPKGLKLEWVANIKODSEKTYVSVKGRFTISRDNANSLYL 120
XX
XX 61 CAASGFTSSYGMHNVROAPKGLKLEWVANIGIFDGNKTYVSVKGRFTISRDNANSLYL 120
XX 121 QMNSLRADDTAVYYCARDLKKVSSSGWF--DPWGRGTYYTVVSSGGSGSGSGSGSGS 178
XX 121 QMNSLRADDTAVYYCARDLKKVSSSGWF--DPWGRGTYYTVVSSGGSGSGSGSGSGSGS 178
XX
XX 121 QMNSLRADDTAVYYCARDLKKVSSSGWF--DPWGRGTYYTVVSSGGSGSGSGSGSGSGS 172
XX 121 QMNSLRADDTAVYYCARDLKKVSSSGWF--DPWGRGTYYTVVSSGGSGSGSGSGSGSGS 172
XX
XX 179 -SELTQDPAVSYALGQTVRITCOGDSLR---SYVASWYQOKPGQAPVLYITGKNNRPSGI 234
XX 179 -SELTQDPAVSYALGQTVRITCOGDSLR---SYVASWYQOKPGQAPVLYITGKNNRPSGI 234
XX
XX 173 QSVLTQPPSVSGAPQORTVITSCGTRSSNIGAGHDVHWYQQLPGTAPKLLITDDSNRPSGV 232
XX 173 QSVLTQPPSVSGAPQORTVITSCGTRSSNIGAGHDVHWYQQLPGTAPKLLITDDSNRPSGV 232
XX
XX 235 PDRFSGSSSGNTASLTITGAQAEADADYVCSNRDSSGNHNVFGGSKTLTVLGAANHHNH 294
XX 235 PDRFSGSSSGNTASLTITGAQAEADADYVCSNRDSSGNHNVFGGSKTLTVLGAANHHNH 294
XX
XX 233 PDRFSGSSSGNTASLTITGAQAEADADYVCSNRDSSGNHNVFGGSKTLTVLGAANHHNH 292
XX 233 PDRFSGSSSGNTASLTITGAQAEADADYVCSNRDSSGNHNVFGGSKTLTVLGAANHHNH 292
XX
XX 295 HGAEOKLISEEDLNGAA 312
XX 295 HGAEOKLISEEDLNGAA 312
XX
XX 293 HGAEOKLISEEDLNGAA 310
XX 293 HGAEOKLISEEDLNGAA 310
XX
XX RESULT 9
XX ABG74386
XX ID ABG74386 standard: Protein; 310 AA.
XX
XX ABG74386;
XX
XX 11-APR-2003 (first entry)
XX
XX Single chain antibody (scfv) fragment 24C4.

```

```

XX
XX Apo-2; tumour necrosis factor family; TNFR; gene therapy;
XX apoptosis; tissue-specific typing; affinity purification;
XX competitive-type receptor binding assay; mouse; 24C4.
XX
XX Mus sp.
XX
XX US2002150985-A1.
XX
XX 17-OCT-2002.
XX
XX 02-NOV-2001; 2001US-0052798.
XX
XX 15-MAY-1997; 97US-046615P.
XX
XX 09-FEB-1998; 98US-074119P.
XX
XX 14-MAY-1998; 98US-0079029.
XX
XX (GETH ) GENENTECH INC.
XX
XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX
XX WPI: 2003-198287/19.
XX
XX N-PSDB; ABX16409.
XX
XX New Apo-2 polypeptides and polynucleotides, useful for inducing
XX apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in
XX quantitative diagnostic assays, or in generating antibodies against
XX Apo-2
XX
XX Example 14; Fig 16; 64pp; English.
XX
XX The invention describes a novel isolated Apo-2 polypeptide. The Apo-2
XX polypeptide is useful for inducing apoptosis in mammalian cells, in vivo
XX or ex vivo gene therapy, in quantitative diagnostic assays, as a control
XX against samples containing unknown quantities of Apo-2, in generating
XX antibodies, in affinity purification techniques, and in competitive-type
XX receptor binding assays when labelled with, for instance, radiolabel,
XX enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a
XX diagnostic for tissue-specific typing. This is the amino acid sequence
XX of the single chain antibody fragment (scfv) 24C4 used in the
XX preparation of anti-apo-2 antibodies.
XX
XX Sequence 310 AA;
XX
XX Query Match 75.0%; Score 1231; DB 24; Length 310;
XX Best Local Similarity 77.7%; Pred. No. 3.3e-74;
XX Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;
XX
XX 1 MTMTSPSGAFLEIFNVKLLFAIPLVPPFYAAPAMAGVOLVSSGGGLVOPGSLRLS 60
XX 1 MTMTSPSGAFLEIFNVKLLFAIPLVPPFYAAPAMAGVOLVSSGGGLVOPGSLRLS 60
XX
XX 61 CAASGFTSSYWMVSWROAPKGLKLEWVANIKODSEKTYVSVKGRFTISRDNANSLYL 120
XX 61 CAASGFTSSYWMVSWROAPKGLKLEWVANIKODSEKTYVSVKGRFTISRDNANSLYL 120
XX
XX 61 CAASGFTSSYGMHNVROAPKGLKLEWVANIGIFDGNKTYVSVKGRFTISRDNANSLYL 120
XX 121 QMNSLRADDTAVYYCARDLKKVSSSGWF--DPWGRGTYYTVVSSGGSGSGSGSGSGS 178
XX 121 QMNSLRADDTAVYYCARDLKKVSSSGWF--DPWGRGTYYTVVSSGGSGSGSGSGSGSGS 178
XX
XX 121 QMNSLRADDTAVYYCARDLKKVSSSGWF--DPWGRGTYYTVVSSGGSGSGSGSGSGSGS 172
XX 121 QMNSLRADDTAVYYCARDLKKVSSSGWF--DPWGRGTYYTVVSSGGSGSGSGSGSGSGS 172
XX
XX 179 -SELTQDPAVSYALGQTVRITCOGDSLR---SYVASWYQOKPGQAPVLYITGKNNRPSGI 234
XX 179 -SELTQDPAVSYALGQTVRITCOGDSLR---SYVASWYQOKPGQAPVLYITGKNNRPSGI 234
XX
XX 173 QSVLTQPPSVSGAPQORTVITSCGTRSSNIGAGHDVHWYQQLPGTAPKLLITDDSNRPSGV 232
XX 173 QSVLTQPPSVSGAPQORTVITSCGTRSSNIGAGHDVHWYQQLPGTAPKLLITDDSNRPSGV 232
XX
XX 235 PDRFSGSSSGNTASLTITGAQAEADADYVCSNRDSSGNHNVFGGSKTLTVLGAANHHNH 294
XX 235 PDRFSGSSSGNTASLTITGAQAEADADYVCSNRDSSGNHNVFGGSKTLTVLGAANHHNH 294
XX
XX 233 PDRFSGSSSGNTASLTITGAQAEADADYVCSNRDSSGNHNVFGGSKTLTVLGAANHHNH 292
XX 233 PDRFSGSSSGNTASLTITGAQAEADADYVCSNRDSSGNHNVFGGSKTLTVLGAANHHNH 292
XX
XX 295 HGAEOKLISEEDLNGAA 312
XX 295 HGAEOKLISEEDLNGAA 312
XX
XX 293 HGAEOKLISEEDLNGAA 310
XX 293 HGAEOKLISEEDLNGAA 310
XX

```


RESULT 10
ABG91841
ID ABG91841 standard; Protein; 277 AA.
XX
XX
AC ABG91841;
XX
DT 04-DEC-2002 (first entry)
XX
XX
DE Human antibody fragment #25.
XX
KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW retemosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; relinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.
XX
PN W0200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US49442.
XX
PR 29-DEC-2000; 2000US-258948P.
PR 29-DEC-2000; 2000US-0751181.
XX
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagel Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H,
PI Szantonon E, Richter T, Amit B, Kooperman L, Feretz T, Levanon A,
XX
DR WPI; 2002-674776/72.

PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer -
XX
Claim 23; Page 233-234; 310pp; English.
55

The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody. Its antigen-binding fragment or its complex comprising at least one antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet adhesion or aggregation, for increasing mortality of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-leukaemia agents, or for decreasing the number of tumour or leukaemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diagnosing and treating diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases, cardiovascular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-protein interactions. This sequence represents a human antibody fragment of the invention.

Sequence 277 AA;

Query Match	72.7%	Score 1194;	DB 23;	Length 277;
Best Local Similarity	85.0%	Pred. No. 8-5e-72;		
Matches 238; Conservative	5;	Mismatches 19;	Indels 18;	Gaps 2

```
QY      33 AAQPMAGVOLVESGGGLVQPGGSLRLSCAASGFTFSYIWMSSVNRQAPGKLEWYANIKQ 92
      ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db      16 AAQPMAGVOLVESGGGVNRPGGSLRLSCAASGFTFDYIGMSWNRQAPGKLEWYSGINW 75
```

[illegible]

```

RESULT 11
ABG92019
ID ABG92019 standard; Protein: 277 AA.
XX
XX ABG92019;
AC
XX
XX
DT 04-DEC-2002 (first entry)
XX
DE Human antibody fragment #203.

```

KM	Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KM	metastasis; hypervariable region; autoimmune disease; thrombosis;
KM	retenostosis; leukaemia; inflammatory disease; cardiovascular disease;
KW	myocardial infarction; retinopathic disease; abnormal platelet function;
KM	sulphated tyrosine-dependent protein-protein interaction.
XX	
XX	
OS	Homo sapiens.
PN	W0200253700-A2.
XX	
PD	11-JUL-2002.

PE 31-DEC-2001; 2001WO-US69442.
 XX
 PR 29-DEC-2000; 2000US-258948P.
 PR 29-DEC-2000; 2000US-0751181.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Lazarovits J, Hagal Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H,
 PI Scañlon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A.
 XX
 DR WPI: 2002-674776/72.

PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer -
 XX
 PS Claim 23; Page 308-309; 310pp; English.

The invention relates to an isolated ep

The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet adhesion or aggregation, for increasing mortality of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-leukaemia agents, or for decreasing the number of tumour or leukaemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diagnosing and

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favour of other
PT cells -
XX
PS Claim 141; Fig 14; 232pp; English.
XX
CC The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention.
XX
SQ Sequence 277 AA;
XX
Query Match 72.7%; Score 1194; DB 23; Length 277;
Best Local Similarity 85.0%; Pred. No. 8.5e-72;
Matches 228; Conservative 7; Mismatches 17; Indels 18; Gaps 3;
XX
QY 33 AAQPMAGVQLVESGGGLYOPGSGSLRSCAASGFTFSYWMVSWRQAPGKLEWVANIKQ 92
Db 16 AAQPMAGVQLVESGGGVYRPGSGSLRSCAASGFTFDYDGMVSWRQAPGKLEWVGINW 75
QY 93 DGESEKTVYDSVKRFTISRDNNAKNSLYLQNNSLRAEDTAVYYCARDLLKKGSSGWFDP 152
Db 76 NGSTGYADSVKRFITSRDNNAKNSLYLQNNSLRAEDTAVYYCAR-----LTHPF-- 126
QY 153 WGRGTVTVYSSGGSGGGSGGSSSELTQDPAVSVALGQTVRTICQDGLSRYSYASWY 212
Db 127 WGGGLTVTVYSSRGGSGGGSGGSSSELTQDPAVSVALGQTVRTICQDGLSRYSYASWY 186
QY 213 QQRPGAPVLYLYGKNNRPSGIPDRFSGSSGNTASLTITGAQAEDEADYYCNSRDSG 272
Db 187 QQRPGAPVLYLYGKNNRPSGIPDRFSGSSGNTASLTITGAQAEDEADYYCNSRDSG 246
QY 273 HYVFGGKTKLTVLGAALHHHHHGAADQKLISEEDLNGAA 312
Db 247 HYVFGGKTKLTVLGA-----AAEQKLISEEDLNGAA 277
XX
RESULT 14
ABP45459 standard; Protein: 247 AA.
XX
AC ABP45459;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Bly5 binding scFv SEQ ID 1470.
XX
XX Bly5; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunomodulator; antitumour;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.

XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ribben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX WPL; 2002-114799/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 2157-2158; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Bly5) polypeptides. Bly5 is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antitumour and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Bly5. The antibodies bind to Bly5
CC and so may be used to detect and quantitate the presence of Bly5 in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Bly5. They may also be
CC administered to treat diseases associated with aberrant Bly5 expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 247 AA;
XX
Query Match 72.6%; Score 1192; DB 23; Length 247;
Best Local Similarity 92.7%; Pred. No. 1e-71;
Matches 228; Conservative 3; Mismatches 15; Indels 0; Gaps 0;
XX
QY 41 VOLVESGGGLYOPGSGSLRSCAASGFTFSYWMVSWRQAPGKLEWVANIKOGSEKYYV 100
Db 2 VOLVQSGGGLVOPGSRSLRSCAASGFTFSYWMVSWRQAPGKLEWVANIKOGSEKYYV 61
QY 101 DSVKGRFTISRDNNAKNSLYLQNNSLRAEDTAVYYCARDLLKKGSSGWFDPGRTTVT 160
Db 62 DSVKGRFTISRDNNAKNSLYLQNNSLRAEDTAVYYCARDLFGYHDAEDINGRGIMVT 121
QY 161 VSSGGGSGGGSGGGSSSELTQDPAVSVALGQTVRTICQDGLSRYSYASWYQQRPGAP 220
Db 122 VSSGGGSGGGSGGGSSSELTQDPAVSVALGQTVRTICQDGLSRYSYASWYQQRPGAP 181
QY 221 VLTVYGNKNNRPSGIPDRFSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNVVGCGT 280
Db 182 VLTVYGNKNNRPSGIPDRFSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNVVGCGT 241
QY 281 KLTVLG 286
Db 242 KLTVLG 247
XX
RESULT 15
ABG92024 standard; Protein: 263 AA.
XX
AC ABG92024;
XX
DT 04-DEC-2002 (first entry)

XX Antibody protein #4.
DE
XX
KW Antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Unidentified.
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US49442.
XX
PR 29-DEC-2000; 2000US-258948P.
PR 29-DEC-2000; 2000US-0751181.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarevits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szantloun E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR WPI; 2002-674776/72.
XX
XX Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer -
XX
PS Disclosure; Fig 50; 310pp; English.
XX
XX The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,
CC platelet-platelet and/or cell-platelet adhesion or aggregation, for
CC increasing mortality of tumour or leukaemia cells, for increasing the
CC susceptibility of diseased cells to damage by anti-disease, anti-cancer
CC or anti-leukaemia agents, or for decreasing the number of tumour or
CC leukaemia cells in a patient, or in the manufacture of a medicament for
CC the above mentioned purposes. The epitopes are useful for diagnosing and
CC treating diseases such as cancer, leukaemia, autoimmune diseases,
CC inflammatory diseases, cardiovascular diseases such as myocardial
CC infarction, retinopathic diseases and other diseases mediated by abnormal
CC platelet function and diseases caused by sulphated tyrosine-dependent
CC protein-protein interactions. This sequence represents an antibody
CC
XX
XX Sequence 263 AA;
SQ

Query Match 72.4%; Score 118; DB 23; Length 263;
Best Local Similarity 86.4%; Pred. No. 2e-71;
Matches 235; Conservative 5; Mismatches 16; Indels 16; Gaps 2;

OY 41 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMQSVROAPGKLEWVANIQRDSEKYYV 100
DB 2 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMQSVROAPGKLEWVSAISGSGSTYYA 61
OY 101 DSVAGRFTISRDNAKNSLYLQMNSLRADTAIVYCCARDLKVKSSSGMFDPKRGRTTYT 160
DB 62 DSVAGRFTISRDNSKNTLYLQMNSLRADTAIVYCCARTGOSIKRS-----WGQGLTYT 114
OY 161 VSSGGGGSGGGSGGSSSETLQDPAYVALGQTVIRITCOGDSLRSYYASWYQKPGQAP 220
DB 115 VSRGGGGSGGGSGGSSSETLQDPAYVALGQTVIRITCOGDSLRSYYASWYQKPGQAP 174

OY 221 VLVIYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYCNRSDDSGNHVFGGCT 280
DB 175 VLVIYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYCNRSDDSGNHVFGGCT 234
OY 281 KLTVLGAHAHHHHHGAAGKLISEEDLNGAA 312
DB 235 KLTVLGA-----AAEQKLISEEDLNGAA 257

Search completed: September 22, 2003, 15:18:44
Job time : 53.2793 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 18.4318 Seconds
(Without alignments)
716.207 Million cell updates/sec

Title: US-10-052-798-10

Perfect score: 1642

Sequence: 1 MTMTTSPFGAFLEIFNVKK.....HHHGAEOKLISEEDLNGAA 312

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1642	100.0	312	4	US-09-079-029-10
2	1460.5	88.9	309	4	US-09-079-029-9
3	1231	75.0	310	4	US-09-079-029-11
4	1176.5	71.7	280	3	US-09-260-527-1
5	1037.5	63.2	278	3	US-09-260-527-3
6	937	57.1	249	4	US-10-039-785-53
7	850.5	51.8	284	3	US-09-184-658-40
8	835	50.9	289	3	US-09-184-658-63
9	827.5	50.4	284	3	US-08-564-164-2
10	819.5	49.9	334	4	US-09-646-028-53
11	819.5	49.9	339	4	US-09-646-028-55
12	815.5	49.7	348	4	US-09-646-028-51
13	802	48.8	245	4	US-08-918-148-78
14	798	48.6	282	2	US-08-860-174-10
15	795.5	48.4	301	2	US-08-661-052-14
16	795.5	48.4	301	3	US-09-188-082-14
17	795.5	48.4	301	4	US-09-364-088-14
18	795.5	48.4	301	4	US-09-102-716-14
19	795	48.4	245	4	US-08-918-148-75
20	792	48.2	225	4	US-09-553-498-8
21	792	48.1	255	4	US-09-618-869-8
22	790.5	48.1	297	4	US-09-486-814-2
23	789	48.1	245	4	US-08-918-148-76
24	778	47.4	359	4	US-09-646-028-16
25	774	47.1	361	4	US-09-646-028-13
26	760.5	46.3	244	4	US-08-918-148-77
27	746	45.4	281	4	US-09-025-769B-178

28	741.5	45.2	553	2	US-08-661-052-16	Sequence 16, App1
29	741.5	45.2	553	3	US-09-188-082-16	Sequence 16, App1
30	741.5	45.2	553	4	US-09-364-088-16	Sequence 16, App1
31	741.5	45.2	553	4	US-09-102-716-16	Sequence 16, App1
32	740.5	45.1	268	4	US-09-554-765-2	Sequence 2, App11
33	739.5	45.0	277	2	US-08-256-790-2	Sequence 2, App11
34	736	44.8	249	4	US-08-918-148-74	Sequence 74, App1
35	733	44.6	258	4	US-08-665-202-5	Sequence 5, App1
36	733	44.6	258	4	US-09-315-574-5	Sequence 5, App1
37	725.5	44.2	244	4	US-08-918-148-79	Sequence 79, App1
38	724	44.1	245	4	US-10-039-785-42	Sequence 42, App1
39	724	44.1	247	3	US-09-227-693-34	Sequence 34, App1
40	724	44.1	248	1	US-08-331-398A-34	Sequence 34, App1
41	724	44.1	248	2	US-08-331-397B-34	Sequence 34, App1
42	724	44.1	248	2	US-08-759-804A-34	Sequence 34, App1
43	721.5	43.9	243	1	US-07-958-140-2	Sequence 2, App11
44	721.5	43.9	243	5	PCT-US93-09166-2	Sequence 2, App11
45	721	43.9	240	1	US-08-488-113B-148	Sequence 148, App

ALIGNMENTS

```
RESULT 1
US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntarapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079, 029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P101R2
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-10
Query Match 100.0%; Score 1642; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTMTTSPFGAFLEIFNVKKLFAIPLVVFYAAOPAMAGVOLVESGGGLVOPGGSLRLS 60
Db 1 MTMTTSPFGAFLEIFNVKKLFAIPLVVFYAAOPAMAGVOLVESGGGLVOPGGSLRLS 60
QY 61 CAASGFTFSSYMSWVRQAPGKGLIEWYANIKDGSSEKYYVDSVKGRTTISRDNKNSLYL 120
```

```
Db 61 CAASGTTSSYMWVROAPGKLEWVANIKODGSEKYYVDSVKGRFTISRDNKNSLYL 120
QY 121 QMNSLRADPTAVYYCARDLKVKSSSGMFDPMGRGRTVTVSSGGGSGGGSGGSSSE 180
Db 121 QMNSLRADPTAVYYCARDLKVKSSSGMFDPMGRGRTVTVSSGGGSGGGSGGSSSE 180
QY 181 LTQDPAVSVALGQVTRITCGDLSRSYASWYQOKPGAPLVLYTGKNNRPSGIPDRFSG 240
Db 181 LTQDPAVSVALGQVTRITCGDLSRSYASWYQOKPGAPLVLYTGKNNRPSGIPDRFSG 240
QY 241 SSSGNTASLTITGAQAEDEADYYCNSRDSGNHHVFGGCTKLTVLGAANHNNHGAEE 300
Db 241 SSSGNTASLTITGAQAEDEADYYCNSRDSGNHHVFGGCTKLTVLGAANHNNHGAEE 300
QY 301 KLISEEDLINGAA 312
Db 301 KLISEEDLINGAA 312
```

RESULT 2

```
US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapal, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079.029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-9
```

```
Query Match 88.9%; Score 1460.5; DB 4; Length 309;
Best Local Similarity 90.1%; Pred. No. 1.4e-11;
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;
```

```
QY 1 MTMTIPSGAFLEIFENVKLLFAIPLVVFPFYAAPAMAVQVLVSSGGGLVQPGGSLRLS 60
Db 1 MTMTIPSGAFLEIFENVKLLFAIPLVVFPFYAAPAMAVQVLVSSGGGLVQPGGSLRLS 60
QY 61 CAASGFTSSYMWVROAPGKLEWVANIKODGSEKYYVDSVKGRFTISRDNKNSLYL 120
Db 61 CAASGFTDDYGMVROAPGKLEWVGINNNGSGTGTADSVKRVITISRDNKNSLYL 120
```

```
QY 121 QMNSLRADPTAVYYCARDLKVKSSSGMFDPMGRGRTVTVSSGGGSGGGSGGSSS 179
Db 121 QMNSLRADPTAVYYCA-----KLTGAGRCWYFDLMGKGTTVTVSSGGGSGGGSGGSSS 176
QY 180 ELTOPAVSVALGQVTRITCGDLSRSYASWYQOKPGAPLVLYTGKNNRPSGIPDRFS 239
Db 177 ELTOPAVSVALGQVTRITCGDLSRSYASWYQOKPGAPLVLYTGKNNRPSGIPDRFS 236
QY 240 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNHHVFGGCTKLTVLGAANHNNHGAEE 299
Db 237 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNHHVFGGCTKLTVLGAANHNNHGAEE 296
QY 300 KLISEEDLINGAA 312
Db 297 KLISEEDLINGAA 309
```

RESULT 3

```
US-09-079-029-11
; Sequence 11, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapal, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079.029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-11
```

```
Query Match 75.0%; Score 1231; DB 4; Length 310;
Best Local Similarity 77.7%; Pred. No. 7.3e-93;
Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;
```

```
QY 1 MTMTIPSGAFLEIFENVKLLFAIPLVVFPFYAAPAMAVQVLVSSGGGLVQPGGSLRLS 60
Db 1 MTMTIPSGAFLEIFENVKLLFAIPLVVFPFYAAPAMAVQVLVSSGGGLVQPGGSLRLS 60
QY 61 CAASGFTSSYMWVROAPGKLEWVANIKODGSEKYYVDSVKGRFTISRDNKNSLYL 120
Db 61 CAASGFIFSSYGMVROAPGKLEWVAGIFYDGNKYYADSVKGRFTISRDNKNSLYL 120
QY 121 QMNSLRADPTAVYYCARDLKVKSSSGMFDPMGRGRTVTVSSGGGSGGGSGGSSS 178
Db 121 QMNSLRADPTAVYYCARD-----KGIYMDVWGKGTITVTVSSGGGSGGGSGGSSS 172
```

```
OY 179 -SELTPDPAVSVALGOTVITCOGDSLR---SYVASWYQOKPGQAPVLYYGNKNNRPSGI 234
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 173 QSVLQPPSVSCAPQQRRTISTCGSSNSNGASHDHWYQOLPTAKLILYDSDNRPSGV 232
OY 235 PDFFSGSSSGNTASLTITGAQAEADADYVCNSRDSGNHVVGGGKTLTVLGAANHHNH 294
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 233 PDFFSGSRSGTSASLTITGAQAEADADYVCQSYDSSLRGSVFGGKTVLGAANHHNH 292
OY 295 HGAEOKLISEEDLNGAA 312
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 293 HGAEOKLISEEDLNGAA 310
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 4

```
US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J. P.
; APPLICANT: Mikkelsen, J. D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DY0019.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
; OTHER INFORMATION: phage display library known as the Synthetic scfv
; OTHER INFORMATION: Library (#1) from the Centre for Protein
; OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
US-09-260-527-1
```

```
Query Match 71.7%; Score 1176.5; DB 3; Length 280;
Best Local Similarity 83.3%; Pred. No. 1.8e-88;
Matches 235; Conservative 7; Mismatches 21; Indels 19; Gaps 3;
```

```
OY 33 AAQPMAGVQLVESGGGLVQPGGSLRLSCAASGFTFSWMSWVQAPKGLIEWYANIKQ 92
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 16 AAQPMAGVQLVESGGGLVQPGGSLRLSCAASGFTFSWMSWVQAPKGLIEWYGRKIS 75
OY 93 --DGSEKYYVDSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCARDLKYKSSSGWF 150
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 KTDGCTDYAAPVKGKRFITSRDLSKNTLYLQNNSLKTEDTAVYYCARKKRKAL----- 128
OY 151 DPMGSGTYYVSSSGGGSGGGSSSELTQDPAVSVALGQTVRITCOGSLSYAS 210
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 129 -RMGCGTLVTVSRGGSGGGSGGGSSSELTQDPAVSVALGQTVRITCOGDSLRSYAS 187
OY 211 WYQQRPGQAPVLYYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYVCNSRDS 270
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 188 WYQQRPGQAPVLYYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYVCNSRDS 247
OY 271 GNHVVFGGKTLTVLGAANHHNHGAEOKLISEEDLNGAA 312
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 248 GNHVVFGGKTLTVLGA-----AAEOKLISEEDLNGAA 280
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 5

```
US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J. P.
; APPLICANT: Mikkelsen, J. D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
```

```
; FILE REFERENCE: DY0019.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 278
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
; OTHER INFORMATION: from a naive phage display library known as the
; OTHER INFORMATION: Synthetic scfv library (#1) from the Centre for
; OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3
```

```
Query Match 63.2%; Score 1037.5; DB 3; Length 278;
Best Local Similarity 74.0%; Pred. No. 3.9e-77;
Matches 211; Conservative 15; Mismatches 32; Indels 27; Gaps 5;
```

```
OY 33 AAQPMAGVQLVESGGGLVQPGGSLRLSCAASGFTF-SSYMSWVQAPKGLIEWYANIK 91
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 16 AAQPMAGVQLVESGGGLVQPGGSLRLSCAASGFTFSSNMWGMWIRQPPKGLIEWYGYI 75
OY 92 QDSSEKYYVDSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCARDLKYKSSSGWFD 151
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 YSGS--TYNPSLSKRYTKMVDTSKNOFSLSSVAVADYAVYICAR-----FH 122
OY 152 P---WGRCTVTVSSSGGGSGGGSSSELTQDPAVSVALGQTVRITCOGSLRSY 207
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 PRYDPMGCGTLTVTSRGGSGGGSGGGSSSELTQDPAVSVALGQTVRITCOGSLRSY 182
OY 208 YASWYQOKPGQAPVLYYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYVCNSR 267
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 YASWYQOKPGQAPVLYYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYVCNSR 242
OY 268 DSSGNHVVFGGKTLTVLGAANHHNHGAEOKLISEEDLNGAA 312
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 243 DSSGNHVVFGGKTLTVLGA-----AAEOKLISEEDLNGAA 278
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 6

```
US-10-039-785-53
; Sequence 53, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
```

```

; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1006f07 scfv
US-10-039-785-53

Query Match
Best Local Similarity 57.1%; Score 937; DB 4; Length 249;
Pred. No. 5,3e-69;
Matches 186; Conservative 20; Mismatches 39; Indels 4; Gaps 3;

QY 41 VLVESGGGLNPGSLRLSCAASGFTSSYMWKRAQPGKLELVANIKQDGSRTYV 100
Db 2 VLVESGGGLVPGGSLRLSCAASGFTSSYAWKRAQPGKLELVANISGGSGSTYYA 61
QY 101 DSVKGFRTISRDNKNSLYLQNMNSLRAEDTAVYYCARD-LLKVGSSGMFDPWGRTYV 159
Db 62 DSVKGFRTISRDNKNSLYLQNMNSLRAEDTAVYYCARDLPGKLELVANISGGSGSTYYA 121
QY 160 TVSSGGGGSGGGGGGGSSSE--LTQDPVAVSVALGQTVRITCGDLSRSTYASWYQQRPG 217
Db 122 TVSSGGGGSGGGGGGGSSSAQSVLTQPPGVSVSPGQAAARITCSGDKLGDKRYASWYQQRPG 181
QY 218 QAPVLYTYGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYVCNSRDSSGNHYVFG 277
Db 182 QSPVLYTYGKNNRPSGIPDRFGSSSGNTATLKTISTQAMDEADYCLAMDSADW-VFG 240
QY 278 GGTGLTVLG 286
Db 241 GGTGLTVLG 249

RESULT 7
US-09-184-658-40
; Sequence 40, Application US/09184658
; Patent No. 6030792
; GENERAL INFORMATION:
; APPLICANT: Ottenness, Ivan G.
; APPLICANT: Mezes, Peter S.
; APPLICANT: Downs, James T.
; APPLICANT: Johnson, Kimberly S.
; TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
; FILE REFERENCE: PC9946-A
; CURRENT APPLICATION NUMBER: US/09/184,658
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/065,423
; EARLIER FILING DATE: 1997-11-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 40
LENGTH: 284
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:9A4 scfv VH -
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)..(22)
OTHER INFORMATION: pcANTAB6 signal peptide: Val at position 1 is most
OTHER INFORMATION: likely the initiator Met.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (23)..(137)
OTHER INFORMATION: 9A4 VH domain.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (138)..(152)
OTHER INFORMATION: 15 amino acid linker.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (153)..(258)
```

```

; OTHER INFORMATION: 9A4 VL domain.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (262)..(267)
; OTHER INFORMATION: His tag.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (271)..(280)
; OTHER INFORMATION: myc tag.
US-09-184-658-40

Query Match
Best Local Similarity 51.8%; Score 850.5; DB 3; Length 284;
Pred. No. 7.1e-62;
Matches 172; Conservative 39; Mismatches 71; Indels 15; Gaps 6;

QY 18 VKKLEPAIFLVYFYFAOAPAMCYOLVESGGGLVPGGSLRLSCAASGFTSSYMWKRA 77
Db 1 MKKLEPAIFLVYFYFAOAPAMQIQLVQSGPELKKGFTYKISCKASGTTFTDYSIHVK 60
QY 78 QAPKGLLEVANIKQDGSSEKYYDVYKGFRTISRDNKNSLYLQNMNSLRAEDTAVYYCAR 137
Db 61 QAPKGLKWMGNINTETGPEPTVADDEKGFATSLTASATAYLQINLNKEDTAVYYCAR 120
QY 138 DLKTVGSSSGMFDPEGRGRTTYTVSSGGGGSGGGGGSS-ELTQDPA-VSVALGQTV 195
Db 121 -----GSLDYVGQGTTLTVSSGGGGSGGGGSDQIVLTQSPFVFASAPGERV 171
QY 196 RITCGDSLRSYIASWYQQRPGQAPVLYTYGKNNRPSGIPDRFGSSSGNTASLTITGAQ 255
Db 172 TMTCSASSSVS-YMYTQQRPGSSPRLIHANSNLASGVYVRRSGGSGSTSLTISRME 230
QY 256 AEDADYVCNSRDSSGNHVPFGGRTKLVGAHHHHHHGAEEQKLISEEDLNGAA 312
Db 231 AEDATYYCQQRNSTR--TFGGGTLEIIT-AAHHHHHHGAEEQKLISEEDLNGAA 284

RESULT 8
US-09-184-658-63
; Sequence 63, Application US/09184658
; Patent No. 6030792
; GENERAL INFORMATION:
; APPLICANT: Ottenness, Ivan G.
; APPLICANT: Mezes, Peter S.
; APPLICANT: Downs, James T.
; APPLICANT: Johnson, Kimberly S.
; TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
; FILE REFERENCE: PC9946-A
; CURRENT APPLICATION NUMBER: US/09/184,658
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/065,423
; EARLIER FILING DATE: 1997-11-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 63
LENGTH: 289
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)..(22)
OTHER INFORMATION: pcANTAB6 signal peptide: Val at position 1 is most
OTHER INFORMATION: likely initiator Met.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (23)..(138)
OTHER INFORMATION: 5109 VH domain.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (139)..(154)
```



```

Query Match      49.9%;   Score 819.5;   DB 4;   Length 334;
Best Local Similarity 61.8%;   Pred. No. 2.9e-59;
Matches 168;   Conservative 23;   Mismatches 62;   Indels 19;   Gaps 6;
QY      33 AAQPMAGVQLVESGGGLVDPGSGIRLSCAASGFFSSYKMNSWVQAQPGKLEEVANIKQ 92
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```
Db 73 AQAAPKSLVQLLESGGGLVQSGSLRLSCVASGLTFSSSAITWVROAPKGLKLEWVSGICF 132
QY 93 DGESEYVYDVSKGRTTISDNKNSLYLOMNSLRADPTAVYICARDLLKVGSSSGWF-- 150
Db 133 SCDTYYADSVKGRFSASRDNSKNTVYLQMNLRPNDAVYFCA-----NNQTNFCL 185
QY 151 DPMGCTVTVYSS--GGGSGGGSGGGGSG--SELTQDPAVVAALGQVYRITCGDSL 205
Db 186 DNMGGCTVTVYSSRGSGGSGGGSGGSGSVLTQPPSVSAAPQRTVITSCGSRSMI 245
QY 206 --SYASWYQOKPGQAPVLYIGKNNRPSGIPDRFSGSSGNTASLTITGAQAEDEADY 263
Db 246 GAGYDVNWYQKPEPTAPKVLITSNRRPSGVPDRSGSGKSISASLATITGLQLEDEGTY 305
QY 264 CNSRDSGNNHVVFGGCTKLTVLGAAGAAHHHHH 295
Db 306 CQCNDSDLSGLWLFGGGCTKLTVL---RHHHHH 334

RESULT 11
US-09-646-028-55
; Sequence 55, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-55

Query Match 49.9%; Score 819.5; DB 4; Length 339;
Best Local Similarity 61.8%; Pred. No. 3e-59; Mismatches 62; Indels 19; Gaps 6;
Matches 168; Conservative 23;

Db 33 AQAAPAGVQLVESGGGLVQPGSLRLSCAASGFTFSYMWVSWVROAPKGLKLEWVANI 92
Db 78 AQAAPKSLVQLLESGGGLVQSGSLRLSCVASGLTFSSSAITWVROAPKGLKLEWVSGISF 137
QY 93 DGESEYVYDVSKGRTTISDNKNSLYLOMNSLRADPTAVYICARDLLKVGSSSGWF-- 150
Db 138 SCDTYYADSVKGRFSASRDNSKNTVYLQMNLRPNDAVYFCA-----NNQTNFCL 190
QY 151 DPMGCTVTVYSS--GGGSGGGSGGGGSG--SELTQDPAVVAALGQVYRITCGDSL 205
Db 191 DNMGGCTVTVYSSRGSGGSGGGSGGSGSVLTQPPSVSAAPQRTVITSCGSRSMI 250
QY 206 --SYASWYQOKPGQAPVLYIGKNNRPSGIPDRFSGSSGNTASLTITGAQAEDEADY 263
Db 251 GAGYDVNWYQKPEPTAPKVLITSNRRPSGVPDRSGSGKSISASLATITGLQLEDEGTY 310
QY 264 CNSRDSGNNHVVFGGCTKLTVLGAAGAAHHHHH 295
Db 311 CQCNDSDLSGLWLFGGGCTKLTVL---RHHHHH 339

RESULT 12
US-09-646-028-51
; Sequence 51, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
```

```
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-51

Query Match 49.7%; Score 815.5; DB 4; Length 348;
Best Local Similarity 62.9%; Pred. No. 6.5e-59;
Matches 166; Conservative 23; Mismatches 56; Indels 19; Gaps 6;

Db 41 VOLVESGGGLVQPGSLRLSCAASGFTFSYMWVSWVROAPKGLKLEWVANI 100
Db 95 VOLVESGGGLVQSGSLRLSCVASGLTFSSSAITWVROAPKGLKLEWVSGISFGDTTYA 154
QY 101 DSVKGRFTTISRDNKNSLYLOMNSLRADPTAVYICARDLLKVGSSSGWF--DPMGRTT 158
Db 155 DSVKGRFSASRDNSKNTVYLQMNLRPNDAVYFCA-----NNQTNFCLDNMGGCTL 207
QY 159 VYVSS--GGGSGGGSGGGGSG--SELTQDPAVVAALGQVYRITCGDSL--SYASW 211
Db 208 VYVSSRGSGGSGGGSGGSGSVLTQPPSVSAAPQRTVITSCGSRSMI 267
QY 212 YQOKPGQAPVLYIGKNNRPSGIPDRFSGSSGNTASLTITGAQAEDEADY 271
Db 268 YQKPEPTAPKVLITSNRRPSGVPDRSGSGKSISASLATITGLQLEDEGTYCQCNDSL 327
QY 272 NHVVFSGGCTKLTVLGAAGAAHHHHH 295
Db 328 SGWLFGGGCTKLTVL---RHHHHH 348

RESULT 13
US-08-918-148-78
; Sequence 78, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 78
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: unknown
; LOCATION: 208
; OTHER INFORMATION: unknown amino acid
US-08-918-148-78

Query Match 48.8%; Score 802; DB 4; Length 245;
Best Local Similarity 64.8%; Pred. No. 5.3e-58;
Matches 164; Conservative 27; Mismatches 52; Indels 10; Gaps 5;
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:16:07 ; Search time 34.5177 Seconds
(without alignments)
1345.823 Million cell updates/sec

Title: US-10-052-798-10

Perfect score: 1642
Sequence: 1 MTMTSPGAFLEIFNVKK.....HHGAAEQKISEDLNGAA 312

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 556269 seqs, 148893369 residues

Total number of hits satisfying chosen parameters: 556269

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PC7_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PC105_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	1642	100.0	312	12	US-10-288-917-10
2	1642	100.0	312	14	US-10-052-798-10
3	1460.5	88.9	309	12	US-10-288-917-9
4	1460.5	88.9	309	14	US-10-052-798-9
5	1231	75.0	310	12	US-10-288-917-11
6	1231	75.0	310	14	US-10-052-798-11
7	1192	72.6	247	11	US-09-880-748-1470
8	1162	70.8	251	11	US-09-880-748-1594
9	1149	70.0	249	11	US-09-880-748-1109
10	1142	69.5	251	11	US-09-880-748-952
11	1139.5	69.3	248	11	US-09-880-748-1189
12	1138.5	69.3	248	11	US-09-880-748-916
13	1134.5	69.1	248	11	US-09-880-748-914
14	1134.5	69.1	248	11	US-09-880-748-914
15	1134	69.1	237	11	US-09-880-748-2112

16	1133.5	69.0	248	11	US-09-880-748-835	Sequence 835, App
17	1133	69.0	237	11	US-09-880-748-2039	Sequence 2039, App
18	1133	69.0	247	11	US-09-880-748-924	Sequence 924, App
19	1132.5	69.0	248	11	US-09-880-748-1323	Sequence 1323, App
20	1132.5	69.0	290	12	US-09-969-748C-2	Sequence 2, Appl1
21	1132.5	69.0	290	12	US-09-949-039-2	Sequence 12, Appl1
22	1127	68.6	247	11	US-09-880-748-1764	Sequence 1764, App
23	1125.5	68.5	240	11	US-09-880-748-1912	Sequence 1912, App
24	1125.5	68.5	296	12	US-09-949-039-75	Sequence 75, Appl
25	1125.5	68.5	296	12	US-09-880-748-2006	Sequence 2006, Appl
26	1125	68.5	237	11	US-09-880-748-1724	Sequence 1724, App
27	1125	68.5	249	11	US-09-880-748-1731	Sequence 1731, App
28	1124.5	68.5	252	11	US-09-880-748-2056	Sequence 2056, App
29	1124	68.5	243	11	US-09-880-748-2013	Sequence 2013, App
30	1123.5	68.4	248	11	US-09-880-748-1931	Sequence 1931, App
31	1123.5	68.4	239	11	US-09-880-748-2035	Sequence 2035, App
32	1122	68.3	239	11	US-09-880-748-1725	Sequence 1725, App
33	1122	68.3	249	11	US-09-880-748-2018	Sequence 2018, App
34	1119	68.1	239	11	US-09-880-748-1703	Sequence 1703, App
35	1119	68.1	247	11	US-09-880-748-1929	Sequence 1929, App
36	1118	68.1	243	11	US-09-880-748-1931	Sequence 1931, App
37	1117.5	68.1	238	11	US-09-880-748-920	Sequence 920, App
38	1117.5	68.1	248	11	US-09-880-748-2022	Sequence 2022, App
39	1117	68.0	239	11	US-09-880-748-2023	Sequence 2023, App
40	1117	68.0	239	11	US-09-880-748-1817	Sequence 1817, App
41	1116	68.0	249	11	US-09-880-748-912	Sequence 912, App
42	1115	67.9	249	11	US-09-880-748-963	Sequence 963, App
43	1115	67.9	249	11	US-09-880-748-2036	Sequence 2036, App
44	1114	67.8	237	11	US-09-880-748-1911	Sequence 1911, App
45	1112	67.7	241	11		

ALIGNMENTS

RESULT 1
US-10-288-917-10
Sequence 10, Application US/10288917
Publication No. US20030148455A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
Ashkenazi, Avi J.
Chuntharapai, Anan
Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/288,917
FILING DATE: 06-NOV. US20030148455A1-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/052798
FILING DATE: 02-NOV-2001
APPLICATION NUMBER: 09/079029
FILING DATE: 14-MAY-1998
APPLICATION NUMBER: 60/074119
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 60/046615
FILING DATE: 15-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-288-917-10

Query Match 100.0%; Score 1642; DB 12; Length 312;
Best Local Similarity 100.0%; Pred. No. 2,8e-109;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTITPSFGAFLEIFNVKKLFAIPLVYFVAAPAMAGVOLVESGGGLVDPGSLRLS 60
DB 1 MMTITPSFGAFLEIFNVKKLFAIPLVYFVAAPAMAGVOLVESGGGLVDPGSLRLS 60
QY 61 CAASGFTFSYMSWYRQAPGKLEWYANIKODSEKYYVDSYKGRFTISRDAKNSLYL 120
DB 61 CAASGFTFSYMSWYRQAPGKLEWYANIKODSEKYYVDSYKGRFTISRDAKNSLYL 120
QY 121 QMNSLRAEDTAVYYCARDLKVKSSSGWEPDPMGRGTTVYSSGGGSGGGSGSSSE 180
DB 121 QMNSLRAEDTAVYYCARDLKVKSSSGWEPDPMGRGTTVYSSGGGSGGGSGSSSE 180
QY 181 LTDDPAVSVALGTVITTCGDSLRSYASWYQOKPGQAPVLYYKNNRPSGIPDRFSG 240
DB 181 LTDDPAVSVALGTVITTCGDSLRSYASWYQOKPGQAPVLYYKNNRPSGIPDRFSG 240
QY 241 SSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTLVLAHHHHHGAAG 300
DB 241 SSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTLVLAHHHHHGAAG 300
QY 301 KLISEEDLNGAA 312
DB 301 KLISEEDLNGAA 312

RESULT 2

US-10-052-798-10
Sequence 10, Application US/10052798
Publication No. US20020150985A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
Ashkenazi, Avi J.
Chuntharapai, Anan
Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/052,798
FILING DATE: 02-NO. US20020150985A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Matschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-052-798-10

Query Match 100.0%; Score 1642; DB 14; Length 312;
Best Local Similarity 100.0%; Pred. No. 2,8e-109;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTITPSFGAFLEIFNVKKLFAIPLVYFVAAPAMAGVOLVESGGGLVDPGSLRLS 60
DB 1 MMTITPSFGAFLEIFNVKKLFAIPLVYFVAAPAMAGVOLVESGGGLVDPGSLRLS 60
QY 61 CAASGFTFSYMSWYRQAPGKLEWYANIKODSEKYYVDSYKGRFTISRDAKNSLYL 120
DB 61 CAASGFTFSYMSWYRQAPGKLEWYANIKODSEKYYVDSYKGRFTISRDAKNSLYL 120
QY 121 QMNSLRAEDTAVYYCARDLKVKSSSGWEPDPMGRGTTVYSSGGGSGGGSGSSSE 180
DB 121 QMNSLRAEDTAVYYCARDLKVKSSSGWEPDPMGRGTTVYSSGGGSGGGSGSSSE 180
QY 181 LTDDPAVSVALGTVITTCGDSLRSYASWYQOKPGQAPVLYYKNNRPSGIPDRFSG 240
DB 181 LTDDPAVSVALGTVITTCGDSLRSYASWYQOKPGQAPVLYYKNNRPSGIPDRFSG 240
QY 241 SSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTLVLAHHHHHGAAG 300
DB 241 SSSGNTASLTITTAQAEDEADYYCNSRDSGNNHVFEGGKTLVLAHHHHHGAAG 300
QY 301 KLISEEDLNGAA 312
DB 301 KLISEEDLNGAA 312

RESULT 3

US-10-288-917-9
Sequence 9, Application US/10288917
Publication No. US20030148455A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
Ashkenazi, Avi J.
Chuntharapai, Anan
Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/288,917
FILING DATE: 06-NO. US20030148455A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/052798
FILING DATE: 02-NOV-2001

APPLICATION NUMBER: 09/079029
FILING DATE: 14-MAY-1998
APPLICATION NUMBER: 60/074119
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 60/046615
FILING DATE: 15-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-288-917-9

Query Match 88.9%; Score 1460.5; DB 12; Length 309;
Best Local Similarity 90.1%; Pred. No. 2.2e-96;
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;
QY 1 MTMTPTSGAFLEIFENYKLLFAIPLVPPYAPAPAGVQLVSGGGLVOPGSLRLS 60
DB 1 MTMTPTSGAFLEIFENYKLLFAIPLVPPYAPAPAEVQLVSGGGERPGSLRLS 60
QY 61 CAASGFTFSYWMVNRQAPGKLEWVANIKODGSEKYYVDSVYKGRFTISRDNKNSLYL 120
DB 61 CAASGFTFDYDGMVNRQAPGKLEWVSGIMNNGSGTGYADSVKGRVYISRDNKNSLYL 120
QY 121 QMNSLRADPTAVYYCARDLKVKGSSSGW-FDPMGRGTVTYVSSGGGGSGGGSGSS 179
DB 121 QMNSLRADPTAVYYCA---KILGARGWYFDLMGKGTVTYVSSGGGGSGGGSGSS 176
QY 180 ELTODPAVVALGOTVRITCGDSLRSYYASMYOQKPGQAPVLVLYGKNNRPSGIPDFRS 239
DB 177 ELTODPAVVALGOTVRITCGDSLRSYYASMYOQKPGQAPVLVLYGKNNRPSGIPDFRS 236
QY 240 GSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEGGTRKLVLYGAAHHHHHGAAE 299
DB 237 GSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEGGTRKLVLYGAAHHHHHGAAE 296
QY 300 OKLISEEDLNGAA 312
DB 297 OKLISEEDLNGAA 309

RESULT 4
US-10-052-798-9
Sequence 9, Application US/10052798
Publication No. US20020150985A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
Ashkenazi, Avi J.
Chuntharapal, Anan
Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/052,798
FILING DATE: 02-NO. US20020150985A1-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-052-798-9

Query Match 88.9%; Score 1460.5; DB 14; Length 309;
Best Local Similarity 90.1%; Pred. No. 2.2e-96;
Matches 282; Conservative 8; Mismatches 18; Indels 5; Gaps 2;
QY 1 MTMTPTSGAFLEIFENYKLLFAIPLVPPYAPAPAGVQLVSGGGLVOPGSLRLS 60
DB 1 MTMTPTSGAFLEIFENYKLLFAIPLVPPYAPAPAEVQLVSGGGERPGSLRLS 60
QY 61 CAASGFTFSYWMVNRQAPGKLEWVANIKODGSEKYYVDSVYKGRFTISRDNKNSLYL 120
DB 61 CAASGFTFDYDGMVNRQAPGKLEWVSGIMNNGSGTGYADSVKGRVYISRDNKNSLYL 120
QY 121 QMNSLRADPTAVYYCARDLKVKGSSSGW-FDPMGRGTVTYVSSGGGGSGGGSGSS 179
DB 121 QMNSLRADPTAVYYCA---KILGARGWYFDLMGKGTVTYVSSGGGGSGGGSGSS 176
QY 180 ELTODPAVVALGOTVRITCGDSLRSYYASMYOQKPGQAPVLVLYGKNNRPSGIPDFRS 239
DB 177 ELTODPAVVALGOTVRITCGDSLRSYYASMYOQKPGQAPVLVLYGKNNRPSGIPDFRS 236
QY 240 GSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEGGTRKLVLYGAAHHHHHGAAE 299
DB 237 GSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEGGTRKLVLYGAAHHHHHGAAE 296
QY 300 OKLISEEDLNGAA 312
DB 297 OKLISEEDLNGAA 309

RESULT 5
US-10-288-917-11
Sequence 11, Application US/10288917
Publication No. US20030148455A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
Ashkenazi, Avi J.
Chuntharapal, Anan
Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/288,917
  FILING DATE: 06-NOV-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 10/052798
  FILING DATE: 02-NOV-2001
  APPLICATION NUMBER: 09/079029
  FILING DATE: 14-MAY-1998
  APPLICATION NUMBER: 60/074119
  FILING DATE: 09-FEB-1998
  APPLICATION NUMBER: 60/046615
  FILING DATE: 15-MAY-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Marschang, Diane L.
  REGISTRATION NUMBER: 35,600
  REFERENCE/DOCKET NUMBER: P1101R2D1C1
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650/225-5416
  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 310 amino acids
    TYPE: Amino Acid
    TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-288-917-11
```

Query Match 75.0%; Score 1231; DB 12; Length 310;
Best Local Similarity 77.7%; Pred. No. 4.5e-80;

Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;

```
OY 1 MTMTIPSGAFLEIFENYKLLFAIPLVPPYAQPAMAGVOLYESGGGLVOPGSLRLS 60
DB 1 MTMTIPSGAFLEIFENYKLLFAIPLVPPYAQPAMAGVOLYESGGGLVOPGSLRLS 60
OY 61 CAASGFTSSYWMNVROAPGKLEWVANIKODSEKYYVSVKGRFTISRDNKNSLYL 120
DB 61 CAASGFTSSYWMNVROAPGKLEWVANIKODSEKYYVSVKGRFTISRDNKNSLYL 120
OY 61 CAASGFTSSYWMNVROAPGKLEWVANIKODSEKYYVSVKGRFTISRDNKNSLYL 120
DB 61 CAASGFTSSYWMNVROAPGKLEWVANIKODSEKYYVSVKGRFTISRDNKNSLYL 120
OY 121 QMNSLRADTAIVYCARLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGSGS 178
DB 121 QMNSLRADTAIVYCARLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGSGS 178
OY 121 QMNSLRADTAIVYCARLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGSGS 178
DB 121 QMNSLRADTAIVYCARLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGSGS 178
OY 179 -SELTQDPAVSAALGQTVRITCOGDSLR---SYASWYQKPGQAPVLVIYKNNRPSGI 234
DB 173 OSVLQPPSVSGAPQGRVTISCTGRSSNIGAGHDVHWYQQLPGRAPKLLIYDSDNRPSGV 232
OY 235 PDRESGSSGNTASLTITGAQAEADYVYCNRSRDSGNNHVVFGGCTKLTVLGAANHHNH 294
DB 233 PDRESGSSGNTASLTITGAQAEADYVYCNRSRDSGNNHVVFGGCTKLTVLGAANHHNH 292
OY 295 HGAAPQKLISEEDLNGAA 312
DB 293 HGAAPQKLISEEDLNGAA 310
```

RESULT 6

```
US-10-052-798-11
Sequence 11, Application US/10052798
Publication No. US20020150985A1
GENERAL INFORMATION:
  APPLICANT: Ashkenazi, Avi J.
              Chutnharapai, Anan
              Kim, Kyung J.
  TITLE OF INVENTION: Apo-2 Receptor
  NUMBER OF SEQUENCES: 14
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Genentech, Inc.
  STREET: 1 DNA Way
  CITY: South San Francisco
```

```
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/052,798
  FILING DATE: 02-NOV-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/079,029
  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
  NAME: Marschang, Diane L.
  REGISTRATION NUMBER: 35,600
  REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650/225-5416
  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 310 amino acids
    TYPE: Amino Acid
    TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-052-798-11
```

Query Match 75.0%; Score 1231; DB 14; Length 310;
Best Local Similarity 77.7%; Pred. No. 4.5e-80;

Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;

```
OY 1 MTMTIPSGAFLEIFENYKLLFAIPLVPPYAQPAMAGVOLYESGGGLVOPGSLRLS 60
DB 1 MTMTIPSGAFLEIFENYKLLFAIPLVPPYAQPAMAGVOLYESGGGLVOPGSLRLS 60
OY 61 CAASGFTSSYWMNVROAPGKLEWVANIKODSEKYYVSVKGRFTISRDNKNSLYL 120
DB 61 CAASGFTSSYWMNVROAPGKLEWVANIKODSEKYYVSVKGRFTISRDNKNSLYL 120
OY 61 CAASGFTSSYWMNVROAPGKLEWVANIKODSEKYYVSVKGRFTISRDNKNSLYL 120
DB 61 CAASGFTSSYWMNVROAPGKLEWVANIKODSEKYYVSVKGRFTISRDNKNSLYL 120
OY 121 QMNSLRADTAIVYCARLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGSGS 178
DB 121 QMNSLRADTAIVYCARLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGSGS 178
OY 121 QMNSLRADTAIVYCARLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGSGS 178
DB 121 QMNSLRADTAIVYCARLWKVSSSGMF--DPMGRGTVTYVSSGGSGSGSGSGSGS 178
OY 179 -SELTQDPAVSAALGQTVRITCOGDSLR---SYASWYQKPGQAPVLVIYKNNRPSGI 234
DB 173 OSVLQPPSVSGAPQGRVTISCTGRSSNIGAGHDVHWYQQLPGRAPKLLIYDSDNRPSGV 232
OY 235 PDRESGSSGNTASLTITGAQAEADYVYCNRSRDSGNNHVVFGGCTKLTVLGAANHHNH 294
DB 233 PDRESGSSGNTASLTITGAQAEADYVYCNRSRDSGNNHVVFGGCTKLTVLGAANHHNH 292
OY 295 HGAAPQKLISEEDLNGAA 312
DB 293 HGAAPQKLISEEDLNGAA 310
```

RESULT 7

```
US-09-880-748-1470
Sequence 1470, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
  APPLICANT: Ruben et al.
  TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly5
  FILE REFERENCE: P523
  CURRENT APPLICATION NUMBER: US/09/880,748
  CURRENT FILING DATE: 2001-06-15
  PRIOR APPLICATION NUMBER: 60/212,210
  PRIOR FILING DATE: 2000-06-15
  PRIOR APPLICATION NUMBER: 60/240,816
  PRIOR FILING DATE: 2000-10-17
```



```
US-09-880-748-952
; Sequence 952, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 952
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-952
```

```
Query Match      70.0%; Score 1149; DB 11; Length 251;
Best Local Similarity 88.8%; Pred. No. 2,4e-74;
Matches 222; Conservative 8; Mismatches 16; Indels 4; Gaps 1;
```

```
OY      41 VOLVESGGGLVQPGGSLRLSCAASGFTFSSTYMSWVRQAPGKGLEWYANIKDGSSEKYYV 100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2 VOLVQSGGGVQPGGSLRLSCAASGFTFSSTYMSWVRQAPGKGLEWYAFIRYDGSNNYYA 61
OY      101 DSVKGRFTISRDNKNSLYLQMSLRAEDPAVYYCADDL-----LKVSGSSSGMFPDPMGRG 156
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      62 DSVKGRFTISRDNKNSLYLQMSLRAEDPAVYYCADDLPPYDILITGYSILTSGMDVWGRG 121
OY      157 TTYVSSGGGGSGGGSGGSSSELTPDPAVSVALGQTVRITTCGDSLRSYASWYQOKP 216
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      122 TLVTVSSGGGGSGGGSGGSSSELTPDPAVSVALGQTVRITTCGDSLRSYASWYQOKP 181
OY      217 GQAPVLYIYGKNNRPSGIPDRFSSSGSNTASLTITGAQADEADYYCNSRDSSGNHYVF 276
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      182 GQAPVLYIYGKNNRPSGIPDRFSSSGSNTASLTITGAQADEADYYCNSRDSSGNHYVF 241
OY      277 GGGTKLTVLG 286
      |||:|||||:
Db      242 GGGTKLTVLG 251
```

```
RESULT 11
US-09-880-748-982
; Sequence 982, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 982
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-982
```

```
Query Match      69.5%; Score 1142; DB 11; Length 251;
Best Local Similarity 88.4%; Pred. No. 7,6e-74;
Matches 221; Conservative 8; Mismatches 17; Indels 4; Gaps 1;
```

```
OY      41 VOLVESGGGLVQPGGSLRLSCAASGFTFSSTYMSWVRQAPGKGLEWYANIKDGSSEKYYV 100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2 VOLVQSGGGVQPGGSLRLSCAASGFTFSSTYMSWVRQAPGKGLEWYAFIRYDGSNNYYA 61
OY      101 DSVKGRFTISRDNKNSLYLQMSLRAEDPAVYYCADDL-----LKVSGSSSGMFPDPMGRG 156
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      62 DSVKGRFTISRDNKNSLYLQMSLRAEDPAVYYCADDLPPYDILITGYSILTSGMDVWGRG 121
OY      157 TTYVSSGGGGSGGGSGGSSSELTPDPAVSVALGQTVRITTCGDSLRSYASWYQOKP 216
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      122 TLVTVSSGGGGSGGGSGGSSSELTPDPAVSVALGQTVRITTCGDSLRSYASWYQOKP 181
OY      217 GQAPVLYIYGKNNRPSGIPDRFSSSGSNTASLTITGAQADEADYYCNSRDSSGNHYVF 276
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      182 GQAPVLYIYGKNNRPSGIPDRFSSSGSNTASLTITGAQADEADYYCNSRDSSGNHYVF 241
OY      277 GGGTKLTVLG 286
      |||:|||||:
Db      242 GGGTKLTVLG 251
```

```
RESULT 12
US-09-880-748-1189
; Sequence 1189, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1189
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1189
```

```
Query Match      69.4%; Score 1139.5; DB 11; Length 256;
Best Local Similarity 87.1%; Pred. No. 1,2e-73;
Matches 222; Conservative 6; Mismatches 18; Indels 9; Gaps 2;
```

```
OY      41 VOLVESGGGLVQPGGSLRLSCAASGFTFSSTYMSWVRQAPGKGLEWYANIKDGSSEKYYV 100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2 VOLVQSGGGVQPGGSLRLSCAASGFTFSSTYMSWVRQAPGKGLEWYAFIRYDGSNNYYA 61
OY      101 DSVKGRFTISRDNKNSLYLQMSLRAEDPAVYYCADDLKVKSSSG-----WDDP 152
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      62 DSVKGRFTISRDNKNSLYLQMSLRAEDPAVYYCADDLKVKSSSG-----WDDP 121
OY      153 WGRGTYTVVSSGGGGSGGGSGGSSSELTPDPAVSVALGQTVRITTCGDSLRSYASWY 212
```

```

Db      122 MGGRTVTVSSGGGGGGGGSSSELTPDPAVSVALGQTVRTTCGDSLRSYASWY 181
Qy      213 QQRPGAPVLYIGKNNRPSGIPDRFSSSGNTASTITGAAEDADYCNSSROSGN 272
Db      182 QQRPGAPVLYIGKNNRPSGIPDRFSSSGNTASTITGAAEDADYCNSSROSGN 241
Qy      273 H-VVFGGRTKLTVLG 286
Db      242 HRGVFGGRTKLTVLG 256

RESULT 13
US-09-880-748-916
; Sequence 916, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 916
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-916

Query Match      69.3%; Score 1138.5; DB 11; Length 248;
Best Local Similarity 88.8%; Pred. No. 1.3e-73;
Matches 221; Conservative 10; Mismatches 13; Indels 5; Gaps 2;

Qy      41 VOLVESGGGLVOPGSGSLRLSCAASGFTFSYMSWVRQAPGKLEWYANIKODSEKYYV 100
Db      2 VOLVESGGGVYOPGSGSLRLSCAASGFTVNSYAMHWRAQAPGKGLQWAVAYISDGSKYYA 61
Qy      101 DSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYICAR---DLKVKSSSGMFPDPMGRGT 157
Db      62 DSVKGRFTYSRDNKNSLYLQMNSLRAEDTAVYICARSHYDIL--TGLNMYEFDLMGRGT 119
Qy      158 TVTVSSGGGGGGGGGGSSSELTPDPAVSVALGQTVRTTCGDSLRSYASWYQOKPG 217
Db      120 TVTVSSGGGGGGGGGGSSSELTPDPAVSVALGQTVRTTCGDSLRSYASWYQOKPG 179
Qy      218 QAPVLYIGKNNRPSGIPDRFSSSGNTASTITGAAEDADYCNSSROSGNHVYFG 277
Db      180 QAPVLYIGKNNRPSGIPDRFSSSGNTASTITGAAEDADYCNSSROSGNHVYFG 239
Qy      278 GGTKLTVLG 286
Db      240 GGTKLTVLG 248

RESULT 14
US-09-880-748-914
; Sequence 914, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523

```

```

; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 914
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-914

Query Match      69.1%; Score 1134.5; DB 11; Length 248;
Best Local Similarity 88.4%; Pred. No. 2.6e-73;
Matches 220; Conservative 10; Mismatches 14; Indels 5; Gaps 2;

Qy      41 VOLVESGGGLVOPGSGSLRLSCAASGFTFSYMSWVRQAPGKLEWYANIKODSEKYYV 100
Db      2 VOLVESGGGVYOPGSGSLRLSCAASGFTVNSYAMHWRAQAPGKGLQWAVAYISDGSKYYA 61
Qy      101 DSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYICAR---DLKVKSSSGMFPDPMGRGT 157
Db      62 DSVKGRFTYSRDNKNSLYLQMNSLRAEDTAVYICARSHYDIL--TGLNMYEFDLMGRGT 119
Qy      158 TVTVSSGGGGGGGGGGSSSELTPDPAVSVALGQTVRTTCGDSLRSYASWYQOKPG 217
Db      120 LTVVSSGGGGGGGGGGSSSELTPDPAVSVALGQTVRTTCGDSLRSYASWYQOKPG 179
Qy      218 QAPVLYIGKNNRPSGIPDRFSSSGNTASTITGAAEDADYCNSSROSGNHVYFG 277
Db      180 QAPVLYIGKNNRPSGIPDRFSSSGNTASTITGAAEDADYCNSSROSGNHVYFG 239
Qy      278 GGTKLTVLG 286
Db      240 GGTKLTVLG 248

RESULT 15
US-09-880-748-2112
; Sequence 2112, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2112
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2112

```

Query Match 69.1%; Score 1134; DB 11; Length 237;
Best Local Similarity 89.4%; Pred. No. 2.7e-73;
Matches 220; Conservative 4; Mismatches 12; Indels 10; Gaps 1;

QY 41 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVSWVROAPGKGLEWVANIKODGSEKYYV 100
|||:|||||
Db 2 VOLVDSGGGLVOPGSLRLSCAASGFTFSYEMNVRQAPGKGLEWVSTISSGSTIYYA 61
|||:|||||

QY 101 DSVKGRFTISRDNANKSLYLQMNLSLAEDTAVYVCARDLLKYKSSSGWFDPWGRGTVT 160
|||:|||||
Db 62 DSVKGRFTISRDNANKSLYLQMNLSLAEDTAVYVCARDT-----DYMGGTRVT 111
|||:|||||

QY 161 VSSGGGGSGGGSSSELTQDPAYVALGQTVARITCGDSLRSYASWTQKPGQAP 220
|||:|||||
Db 112 VSSGGGGSGGGSSSELTQDPAYVALGQTVARITCGDSLRSYASWTQKPGQAP 171
|||:|||||

QY 221 VLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNSRDSGNNHYVFGGT 280
|||:|||||
Db 172 VLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNSRDSGNNHYVFGGT 231
|||:|||||

QY 281 KLTVLG 286
|||:|||||
Db 232 KLTVLG 237
|||:|||||

Search completed: September 22, 2003, 15:36:24
Job time : 35.5177 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 21.1128 seconds
(without alignments)
1421.159 Million cell updates/sec

Title: US-10-052-798-10

Perfect score: 1642

Sequence: 1 MTWITPSFGAFLEIFNVK.....HHHGAEROKLISEEDLNGAA 312

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_76:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	714.5	43.5	268	2	A56446	Ig heavy chain V r
2	578	35.2	249	2	S41374	Single chain Fv an
3	568	34.6	109	2	S19663	Ig lambda chain V
4	562	34.2	108	2	S47184	Ig lambda chain -
5	561	34.2	122	2	S31675	Ig heavy chain V r
6	559	34.0	147	2	I37780	Ig variable region
7	556	33.9	136	2	S31587	Ig heavy chain V r
8	552.5	33.6	117	2	S78486	Ig heavy chain V r
9	551.5	33.6	110	2	S36272	Ig lambda chain V
10	546.5	33.3	139	2	I37781	Ig variable region
11	546	33.3	127	2	S70444	Ig lambda chain pr
12	541	32.9	108	2	S38498	Ig lambda chain -
13	539	32.8	109	2	S38496	Ig lambda chain -
14	530	32.3	233	2	S25748	Ig lambda chain -
15	530	32.3	233	2	JC5322	p3 specific singl
16	527	32.1	108	1	L3H05H	Ig lambda chain V-
17	522.5	31.8	123	2	S31509	Ig heavy chain - h
18	518.5	31.6	110	2	S19672	Ig lambda chain V-
19	517.5	31.5	146	2	S02083	Ig lambda chain V-
20	511	31.1	114	2	S36280	Ig heavy chain V r
21	511	31.1	140	2	S70442	Ig heavy chain pre
22	510.5	31.1	140	2	S22657	Ig heavy chain V r
23	510	31.1	98	2	PL0123	Ig heavy chain V-I
24	510	31.1	117	2	S17079	Ig heavy chain V-g
25	509	31.0	110	2	PH1655	Ig heavy chain V r
26	505	30.8	122	2	E36005	Ig heavy chain V r
27	505	30.8	128	2	S26790	Ig heavy chain V r
28	504.5	30.7	119	2	D36005	Ig heavy chain V r
29	504	30.7	128	2	S26786	Ig heavy chain V r

30	503	30.6	96	2	S36060	Ig lambda chain -
31	503	30.6	115	2	S13726	Ig lambda chain V
32	502.5	30.6	121	2	S19666	Ig heavy chain V r
33	502	30.6	233	2	S25741	Ig lambda chain -
34	497.5	30.3	121	2	G36005	Ig heavy chain V r
35	497	30.3	128	2	S48797	Ig heavy chain V r
36	496	30.2	97	2	PH0872	Ig heavy chain V r
37	496	30.2	114	2	S46390	Ig heavy chain V r
38	495.5	30.2	119	2	F36005	Ig heavy chain V r
39	495	30.1	139	2	S31674	Ig heavy chain V r
40	494.5	30.1	135	2	S31598	Ig heavy chain V r
41	494	30.1	120	2	S48798	Ig heavy chain V r
42	494	30.1	122	2	S31117	Ig heavy chain - h
43	493.5	30.1	132	2	S31603	Ig heavy chain V r
44	493	30.0	141	2	S31669	Ig heavy chain V r
45	492.5	30.0	119	2	C36005	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)

C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C:Accession: A56446

R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity dioxin-binding protein displayed on M13 is functionally ide

A:Reference number: A56446; MUID:95229583; PMID:7713873

A:Accession: A56446

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-268 <TRAN>

A:Cross-references: GB:U20617

C:Keywords: heterotetramer; immunoglobulin

Query Match 43.5%; Score 714.5; DB 2: Length 268;

Best Local Similarity 53.1%; Pred. No. 1.4e-41;

Matches 147; Conservative 38; Mismatches 81; Indels 11; Gaps 5;

Oy	38	MAGVOLVSSGGGLVPGGSLRLSCAASGFTFSYWMGVROAPGKLEWVNIKDGSEK	97
Db	1	MAQVKLOESGAEIVKPGASVSLCTTSGFNKIDTYMMHVKRPPGEGLEIRIAPANGIT	60
Oy	98	YYVDVYKGRFTISDNKNSLYIQMNSLRADTAIVYCCARDLKVKGSSGMPDPWGRGT	157
Db	61	KYDPKFOGKATIAADTSNTAVYQLSSLSLSEDFAVVYCASVYL-----TRYENVWGCGT	114
Oy	158	TVTVSSGGGSGGSGGSGGSS-ELTQDPAY-STALGQTVITTCQGDLSRSTVSWIQOK	215
Db	115	TVTVSSGGGSGGSGGSGGSDIELTQSPALMSASLEKVTMSCRASSSV-FTYVQOK	173
Oy	216	PGQAPVLYIYGCIRPDRFGSSSSGNTASTLTITGAQADADYVCNSRDSSGNHV	275
Db	174	SDASPKLVYTTSHLPQGVPRARFSGSGSGNYSLTISMEEDDAITTCQGFSS--PFT	231
Oy	276	FGGQTKLVIGAAAHNNHNGAEOKLISEEDLNGAA	312
Db	232	FGSGTKLEIKRSAAHNNHNGAEOKLISEEDLNGAA	268

RESULT 2

S41374
single chain Fv antibody - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C:Accession: S41374

R:Artsaenko, O.; Weller, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A:Description: Construction and functional characterization of a single chain Fv anti

F:28-111/Domain: immunoglobulin homology <IMM>

Query Match 34.0%; Score 559; DB 2; Length 147;

Best Local Similarity 80.0%; Pred. No. 2.7e-31;

Matches 108; Conservative 5; Mismatches 8; Indels 14; Gaps 2;

QY 41 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVWVROAPGKLEWVANIKODGSEKYYV 100
 |||||
 DB 15 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVWVROAPGKLEWVANIKODGSEKYYA 74
 |||||
 QY 101 DSVKGRFTISRDNKNSLYLQMNLSLRADTAIVYCARDLKVKSSGMPDPWGRTVT 153
 |||||
 DB 75 DSVKGRFTISRDNKNSLYLQMNLSLRADTAIVYCARDLKVKSSGMPDPWGRTVT 127
 |||||
 QY 154 GRTFTVYSSGSGS 168
 |||||
 DB 128 GCGTTVYSSGSGSASA 142

RESULT 7

S31587

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31587

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31587

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-136 <CUI>

A:Cross-references: EMBL:Z14189; NID:g31005; PIDD:CAA76558.1; PID:g31006

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:31-114/Domain: Immunoglobulin homology <IMM>

Query Match 33.9%; Score 556; DB 2; Length 136;

Best Local Similarity 86.6%; Pred. No. 3.9e-31;

Matches 109; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

QY 41 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVWVROAPGKLEWVANIKODGSEKYYV 100
 |||||
 DB 18 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVWVROAPGKLEWVANIKODGSEKYYV 77
 |||||
 QY 101 DSVKGRFTISRDNKNSLYLQMNLSLRADTAIVYCARDLKVKSSGMPDPWGRTVT 160
 |||||
 DB 78 DSVKGRFTISRDNKNSLYLQMNLSLRADTAIVYCARDLKVKSSGMPDPWGRTVT 133
 |||||
 QY 161 VSS 163
 |||||
 DB 134 VSS 136

RESULT 8

S78486

Ig heavy chain V region (clone FLJ3-28) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000

C:Accession: S78486; S31115

R:Raaphorst, F.M.

submitted to the EMBL Data Library, October 1991

A:Reference number: S78486

A:Accession: S78486

A:Molecule type: mRNA

A:Residues: 1-117 <RA>

A:Cross-references: EMBL:X62965

A:Experimental source: clone FLJ3-28

R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman

Eur. J. Immunol. 22, 247-251, 1992

A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple

A:Reference number: S31104; MUID:92111633; PMID:1730252

A:Accession: S31115

A:Molecule type: mRNA

A:Residues: 1-4,'L','G','34-52,'E','54-73,'K','75-97 <RA>

A:Cross-references: EMBL:X62965

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 33.6%; Score 552.5; DB 2; Length 117;

Best Local Similarity 87.8%; Pred. No. 5.8e-31;

Matches 108; Conservative 2; Mismatches 6; Indels 7; Gaps 1;

QY 41 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVWVROAPGKLEWVANIKODGSEKYYV 100
 |||||
 DB 2 VOLVESGGGLVOPGSLRLSCAASGFTFSYWMVWVROAPGKLEWVANIKODGSEKYYV 61
 |||||
 QY 101 DSVKGRFTISRDNKNSLYLQMNLSLRADTAIVYCARDLKVKSSGMPDPWGRTVT 160
 |||||
 DB 62 DSVKGRFTISRDNKNSLYLQMNLSLRADTAIVYCARDLKVKSSGMPDPWGRTVT 114
 |||||
 QY 161 VSS 163
 |||||
 DB 115 VSS 117

RESULT 9

S36272

Ig lambda chain V region (clone alpha-THY-29) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C:Accession: S36272

R:Griffiths, A.D.; Malmqvist, M.; Marke, J.D.; Bye, J.M.; McCallum, M.J.; McCafferty,

EMBO J. 12, 725-734, 1993

A:Title: Human anti-self antibodies with high specificity from phage display libraries

A:Reference number: S36236; MUID:93178448; PMID:7679990

A:Accession: S36272

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-110 <GR>

A:Cross-references: EMBL:Z18833; NID:g33419; PIDD:CAA79285.1; PID:g939912

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:15-89/Domain: Immunoglobulin homology <IMM>

Query Match 33.6%; Score 551.5; DB 2; Length 110;

Best Local Similarity 98.2%; Pred. No. 6.4e-31;

Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 178 SSELTPDPAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLYIGKNNRPSGIPDR 237
 |||||
 DB 1 SSELTPDPAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLYIGKNNRPSGIPDR 60
 |||||
 QY 238 FSGSSGNTASLTITGAQAEDEADYCNRSRSSGN-HVFGGKTLFVLG 286
 |||||
 DB 61 FSGSSGNTASLTITGAQAEDEADYCNRSRSSGNLYVFGGKTLFVLG 110
 |||||

RESULT 10

I37781

Ig variable region (VDJ) (clone T21-9) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999

C:Accession: I37781; S25475

R:Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A:Title: Somatic diversification in the heavy chain variable region genes expressed b

A:Reference number: A36876; MUID:94119917; PMID:8290556

A:Accession: I37781

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-139 <RES>

A:Cross-references: EMBL:X67908; NID:g33580; PIDD:CAA48106.1; PID:g33581

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

F:35-118/Domain: immunoglobulin homology <IMM>

Query Match 33.3%; Score 546.5; DB 2; Length 139;
Best Local Similarity 87.0%; Pred. No. 1.8e-30;
Matches 107; Conservative 3; Mismatches 8; Indels 5; Gaps 1;

QY 41 VOLVESGGILNPGGSLRLSCAASGFTSSYMSWRQAPGKLEWVANIKODGSKYYV 100
|||||
DB 22 VOLVESGGILNPGGSLRLSCAASGFTSSYMSWRQAPGKLEWVANIKODGSKYYV 81
QY 101 DSVKGFRTISRDAKSLYLQMNSLRAEDTAAYYCARDLLKYVSSSGWFDPWGRTPTV 160
|||||
DB 82 DSVKGFRTISRDAKSLYLQMNSLRAEDTAAYYCAR-----KRAKAAFNITGQTMVT 136
QY 161 VSS 163
|||
DB 137 VSS 139

RESULT 11

Ig lambda chain precursor V region - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C:Accession: S70444; S70426
R:CluSinter, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A:Title: Igm kappa/lambda EBV human B cell clone: an early step of differentiation of B
A:Reference number: S70442; MUID:93024508; PMID:1383695
A:Accession: S70444
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-127 <CUI>
A:Experimental source: clone E29.1
R:Tonnelle, C.
submitted to the EMBL Data Library, May 1990
A:Reference number: S70426
A:Accession: S70426
A:Molecule type: mRNA
A:Residues: 1-90 <TON>
A:Cross-references: EMBL:X53070
A:Experimental source: cell line E29.1, clone VL 29-1
C:Superfamily: immunoglobulin V region: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>
F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 33.3%; Score 546; DB 2; Length 127;
Best Local Similarity 97.2%; Pred. No. 1.7e-30;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 178 SSELTDPAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYTYGKNRPSGIPDR 237
|||||
DB 20 SSELTDPAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYTYGKNRPSGIPDR 79
QY 238 FSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGKTLVL 285
|||||
DB 80 FSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGKTLVL 127

RESULT 12

Ig lambda chain - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S38498
R:Harks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finneer, R.; Gorlick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a B
A:Reference number: S38488
A:Accession: S38498
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-108 <MAR>
A:Cross-references: EMBL:Z23035; NID:9414043; PIDN:CAA80570.1; PID:9414044
C:Superfamily: immunoglobulin V region: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 32.9%; Score 541; DB 2; Length 108;
Best Local Similarity 97.2%; Pred. No. 3.2e-30;
Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 179 SSELTDPAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYTYGKNRPSGIPDR 238
|||||
DB 1 SSELTDPAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYTYGKNRPSGIPDR 60
QY 239 FSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGKTLVLG 286
|||||
DB 61 FSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGKTLVLG 108

RESULT 13

Ig lambda chain - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S38496
R:Harks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finneer, R.; Gorlick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from
A:Reference number: S38488
A:Accession: S38496
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <MAR>
A:Cross-references: EMBL:Z23031; NID:9414039; PIDN:CAA80566.1; PID:9414040
C:Superfamily: immunoglobulin V region: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-88/Domain: immunoglobulin homology <IMM>

Query Match 32.8%; Score 539; DB 2; Length 109;
Best Local Similarity 93.6%; Pred. No. 4.4e-30;
Matches 102; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 178 SSELTDPAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYTYGKNRPSGIPDR 237
|||||
DB 1 SSELTDPAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYTYGKNRPSGIPDR 60
QY 238 FSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGKTLVLG 286
|||||
DB 61 FSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGKTLVLG 109

RESULT 14

Ig lambda chain - human

C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25748
R:Combratio, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25748
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-233 <COM>
A:Cross-references: EMBL:X57813; NID:933725; PIDN:CAA40950.1; PID:933726
C:Superfamily: immunoglobulin V region: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 32.3%; Score 530; DB 2; Length 233;
Best Local Similarity 91.7%; Pred. No. 4e-29;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:03 ; Search time 11.7293 Seconds

(without alignments)
1250.910 Million cell updates/sec

Title: US-10-052-798-10

Perfect score: 1642

Sequence: 1 MTMTIPSGAFLLEIFNVKK.....HHGADEQKLISEDLNGAA 312

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	527	32.1	108	1	LV3A_HUMAN
2	468	28.5	116	1	HV3T_HUMAN
3	454	27.6	122	1	HV3G_HUMAN
4	447	27.2	114	1	HV3B_HUMAN
5	446	27.2	126	1	HV3K_HUMAN
6	437	26.6	119	1	HV38_MOUSE
7	436.5	26.6	121	1	HV3J_HUMAN
8	433	26.4	117	1	HV3C_HUMAN
9	430.5	26.2	119	1	HV3I_HUMAN
10	429	26.1	122	1	HV3H_HUMAN
11	427.5	26.0	115	1	HV3F_HUMAN
12	427	26.0	136	1	HV16_MOUSE
13	418.5	25.5	115	1	HV3D_HUMAN
14	418.5	25.5	123	1	HV18_MOUSE
15	418	25.5	119	1	HV3M_HUMAN
16	418	25.5	119	1	HV3N_HUMAN
17	417	25.4	111	1	HV35_MOUSE
18	416.5	25.4	116	1	HV05_CARAU
19	416.5	25.4	142	1	HV01_RAT
20	414.5	25.2	123	1	HV19_MOUSE
21	414	25.2	122	1	HV20_MOUSE
22	414	25.2	122	1	HV3A_HUMAN
23	413.5	25.2	123	1	HV25_MOUSE
24	413	25.2	119	1	HV37_MOUSE
25	413	25.2	122	1	HV21_MOUSE
26	412.5	25.1	120	1	HV3E_HUMAN
27	412	25.1	119	1	HV40_MOUSE
28	411.5	25.1	117	1	HV41_MOUSE
29	410.5	25.0	113	1	HV23_MOUSE
30	410	25.0	127	1	HV54_MOUSE
31	409	24.9	120	1	HV3U_HUMAN
32	406.5	24.8	113	1	HV30_MOUSE
33	406.5	24.8	115	1	HV32_MOUSE

34	406	24.7	114	1	HV01_CANFA	P01784 canis fam11
35	405.5	24.7	118	1	HV39_MOUSE	P01809 mus musculu
36	405	24.7	98	1	HV57_MOUSE	P18528 mus musculu
37	402.5	24.5	113	1	HV31_MOUSE	P01800 mus musculu
38	402.5	24.5	123	1	HV26_MOUSE	P01791 mus musculu
39	401.5	24.5	144	1	HV26_MOUSE	P01791 mus musculu
40	400.5	24.4	119	1	HV31_HUMAN	P01773 homo sapien
41	399.5	24.3	113	1	HV27_MOUSE	P01796 mus musculu
42	399.5	24.3	123	1	HV24_MOUSE	P01793 mus musculu
43	399	24.3	117	1	HV55_MOUSE	P18526 mus musculu
44	396	24.1	115	1	HV3S_HUMAN	P01780 homo sapien
45	395.5	24.1	97	1	HV56_MOUSE	P18527 mus musculu

ALIGNMENTS

RESULT 1					ALIGNMENTS				
ID	LV3A_HUMAN	STANDARD:	PRT:	108 AA.					
AC	P01714:								
DT	21-JUL-1986 (Rel. 01, Created)								
DT	21-JUL-1986 (Rel. 01, Last sequence update)								
DT	15-SEP-2003 (Rel. 42, Last annotation update)								
DE	Ig lambda chain V-II region SH.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;								
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE.								
RX	MEDLINE=70166723; PubMed=490564;								
RA	Titani K., Wikler M., Shindoda T., Putnam F.W.;								
RT	The amino acid sequence of a lambda type Bence-Jones protein. 3. The								
RT	complete amino acid sequence and the location of the disulfide								
RT	bridges.";								
RL	J. Biol. Chem. 245:2171-2176(1970).								
CC	1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.								
CC	1- SIMILARITY: Contains 1 immunoglobulin-like domain.								
DR	PIR: A01980; L3HUSH.								
DR	HSSP: P80748; 2LOI.								
DR	GO: GO:0005576; C:extracellular; NAS.								
DR	GO: GO:0003823; F:antigen binding activity; NAS.								
DR	GO: GO:0006955; P:immune response; NAS.								
DR	InterPro: IPR007110; Ig-like.								
DR	InterPro: IPR003006; Ig_MHC.								
DR	InterPro: IPR003596; Ig_V.								
DR	Pfam: PF00047; Ig_1.								
DR	SMART: SM00406; IGV; 1.								
DR	PROSITE: PS50835; IG_LIKE; 1.								
KW	Immunoglobulin V region; Bence-Jones protein.								
FT	DOMAIN 1 97								
FT	DISULFID 21 86								
FT	NON_TER 108								
SEQUENCE	108 AA: 11392 MW; E7E1229586411A56 CRC64;								
Query Match									
Best Local Similarity 32.1%; Score 527; DB 1; Length 108;									
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;									
QY	179	SETLDDPAVSVALGQTVRITCGDLSRSYYSWYQKPGQAPVLVIYKKNRPSGIPRF	238						
DB	1	SETLDDPAVSVALGQTVRITCGDLSRGTDAWYQKPGQAPVLVIYKKNRPSGIPRF	60						
QY	239	SGSSSGNATSLTTTGAQAEADADYYCNSRDSSGNHVFGGKTLTVLG	286						
DB	61	SGSSSGNATSLTTTGAQAEADADYYCNSRDSSGKHYLFGGKTLTVLG	108						
RESULT 2									
ID	HV3T_HUMAN	STANDARD:	PRT:	116 AA.					
AC	P01781:								

```

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=75059123; PubMed=4803843;
RA Matanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT type), subgroup H III. Architecture of the complete IgM-molecule.";
RT Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN [2]
RP REVISION TO 28-33.
RA Hilschmann N.;
RL Submitted (JUN-1975) to the PIR data bank.
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
CC PIR: A02064; M3HUGL.
DR HSSP: P01772; 2F84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match 28.5%; Score 468; DB 1; Length 116;
Best Local Similarity 74.4%; Pred. No. 2e-27;
Matches 93; Conservative 8; Mismatches 12; Indels 12; Gaps 2;

QY 41 VOLVESGGGLVPGGSLRLSCAASGFTFSYWMYRWAPGKLEWVANIKODGSEKYYV 100
DB 2 VELVESGGGLVPGGSLRLSCAASGFTFSYWMYRWAPGKLEWVANIKODGSEKYYV 61
QY 101 DSVKGRFTISRDNKASLTLYLQNSLRPEPTAVYYCARDLLKYGSSSGW--PDPMGRGT 158
DB 62 DSVKGRFTISRDNKASLTLYLQNSLRPEPTAVYYCARDLLKYGSSSGW--PDPMGRGT 111
QY 159 VTWSS 163
DB 112 VTWST 116

RESULT 3
HY3G_HUMAN STANDARD; PRT; 122 AA.
ID HV3G_HUMAN
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:

```

```

RT location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02051; M3HUM.
DR HSSP: P01772; 2F84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyrolydione carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D352P1C2 CRC64;

Query Match 27.6%; Score 454; DB 1; Length 122;
Best Local Similarity 71.5%; Pred. No. 2.1e-26;
Matches 88; Conservative 15; Mismatches 18; Indels 2; Gaps 2;

QY 41 VOLVESGGGLVPGGSLRLSCAASGFTFSYWMYRWAPGKLEWVANIKODGSEKYYV 100
DB 2 VELVESGGGLVPGGSLRLSCAASGFTFSYWMYRWAPGKLEWVANISVGBBKYYA 61
QY 101 DSVKGRFTISRDNKASLTLYLQNSLRPEPTAVYYCARDLLKYGSSSGWFDPMGRGT 160
DB 62 DSVKGRFTISRDNKASLTLYLQNSLRPEPTAVYYCARD--RPLYGBYRA-FNYWGGGLTVT 119
QY 161 VSS 163
DB 120 VSS 122

RESULT 4
HY3G_HUMAN STANDARD; PRT; 114 AA.
ID HV3G_HUMAN
AC P01763;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";
RT Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02046; M3HWE.
DR HSSP: P01772; 2F84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.

```

FT	DISULFID	22	96
FT	DISULFID	105	110
FT	STRAND	3	7
FT	STRAND	11	12
FT	TURN	14	15
FT	STRAND	18	25

RP SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudikoff S., Kruttsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating regions."
RT complementarity-determining regions.";
CC Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN.
CC THAT BINDS GALACTAN.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02078; AYWST6.
DR HSSP; P01810; 2EBJ.
DR InterPro; IPR007110; Ig_1-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_Like; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.


```

DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
DR PROSITE: PS50835; 1g-LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 111
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DC64 CRC64;

Query Match
Best Local Similarity 26.0%; Score 427.5; DB 1; Length 115;
Matches 84; Conservative 17; Mismatches 13; Indels 9; Gaps 2;

QY 41 VOLVESGGGLVPGGSLRLSCAASGFTFSYMMSWVRQAPGKGLVNAVITKQDSEKYYV 100
DB 2 VOLVESGGGLVPGGSLRLSCAASGFTVSBMSWVRQAPGKALZWVSALYRGRT--TYVA 60
QY 101 DSVKGRFTISRDNKASLYLQNSLRLEDAEDTAVYYCARDLLKYKSSSGMFDPRGRTYY 160
DB 61 DSVKGRFTISRDRSRRTVYLQMSLRLEDAEDTAVYYCARDLAAR-----LFGKRTYY 112
QY 161 VSS 163
DB 113 VSS 115

RESULT 12
HV16_MOUSE
ID HV16_MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adelung K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: J00522; AAD15290.1; -.
DR PIR: E90809; GIMS21.
DR PDB: 1IGC; 03-JUN-95.
DR InterPro: IPR007110; 1g_1like.
DR InterPro: IPR003006; 1g_MHC.
DR InterPro: IPR003596; 1g_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
DR PROSITE: PS50835; 1g-LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT NON_TER 1 1
FT SIGNAL <1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.

```

```

FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78
FT CONFLICT 89 90
FT CONFLICT 115 115
FT CONFLICT 120 120
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDF7016 CRC64;

Query Match
Best Local Similarity 26.0%; Score 427; DB 1; Length 136;
Matches 86; Conservative 10; Mismatches 16; Indels 18; Gaps 2;

QY 41 VOLVESGGGLVPGGSLRLSCAASGFTFSYMMSWVRQAPGKGLVNAVITKQDSEKYYV 100
DB 18 VOLVESGGGLVPGGSRKLSCAASGFTFSFGHNWVRQAPGKGLVNAVITSSGSLHYA 77
QY 101 DSVKGRFTISRDNKASLYLQNSLRLEDAEDTAVYYCARDLLKYKSSSGM-----FDPW 153
DB 78 DSVKGRFTISRDNKNTFLQMTSLRSEDTAVYYCAR-----WGNYPYAMDYW 126
QY 154 GGGTYTVSS 163
DB 127 GGSTVTVSS 136

RESULT 13
HV3D_HUMAN
ID HV3D_HUMAN STANDARD; PRT; 115 AA.
AC P01765;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-JII region TIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78005528; PubMed=409716;
RA Wang A.-C., Wang I.Y., Fudenberg H.H.;
RT "Immunoglobulin structure and genetics. Identity between variable
RT regions of a mu and a gamma2 chain.";
RL J. Biol. Chem. 252:7192-7199(1977).
CC
CC -1- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
CC OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
CC IDENTICAL.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02048; H3HUTL.
DR HSP: P01772; 2F84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; 1g_1like.
DR InterPro: IPR003006; 1g_MHC.
DR InterPro: IPR003596; 1g_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
DR PROSITE: PS50835; 1g-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 108
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12356 MW; 4DC67D179F62326 CRC64;

Query Match
Best Local Similarity 25.5%; Score 418.5; DB 1; Length 115;
Matches 86; Conservative 12; Mismatches 15; Indels 11; Gaps 3;

QY 41 VOLVESGGGLVPGGSLRLSCAASGFTFSYMMSWVRQAPGKGLVNAVITKQDSEKYYV 100

```



```
Db 2 VOLLESGGGLVOPGSGRLSCAASGFTFSSYVMSWVRQAPGKGLZWNVAIGZLSVSZSYA 61
Oy 101 DSVKGRFTISRDNKNSLYLQWNSLRAEDTAVVYCCARDLKKVKS--SSGWFDDPGRGTTY 159
Db 62 BSKVGRFTISRDNKNSLT---MNSLRADTAIVYICA-----KGVSAIYFBYWGZGTLV 111
Oy 160 TVSS 163
Db 112 TVSS 115

RESULT 14
HV18_MOUSE
ID HV18_MOUSE STANDARD; PRT; 123 AA.
AC P01787;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (TEPC 15).
RX MEDLINE=76222762; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
RT phosphorylcholine-binding proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
RN [2]
RP SEQUENCE FROM N.A. (H107).
RX MEDLINE=80199926; PubMed=6769593;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
RT three segments of DNA: VH, D and JH."
RL Cell 19:981-992(1980).
RN [3]
RP SEQUENCE (S107).
RX MEDLINE=76110488; PubMed=813561;
RA Rudikoff S., Barsstad P., Potter M., Hood L.;
RL Unpublished results, cited by:
RL Hood L., Campbell J.H., Elgin S.C.R.;
RL Annu. Rev. Genet. 9:305-353(1975).
RN [4]
RP SEQUENCE (HPCM1, HPCM2 AND HPCM3).
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
RT their IgM counterparts."
RL Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.
CC -1- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MELDOMA AND
CC HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A93804; AVMST5.
DR HSSP: P01789; IMCP.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; IG-LIKE; 1.
KM Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 114 IG-LIKE.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;

Query Match 25.5%; Score 418.5; DB 1; Length 123;
Best Local Similarity 66.4%; Pred. No. 7.9e-24;
Matches 83; Conservative 14; Mismatches 23; Indels 5; Gaps 2;

Oy 41 VOLVESGGGLVOPGSGRLSCAASGFTFSSYVMSWVRQAPGKGLZWNVAIKQDSCSE--Ky 98
```

```
Db 2 VKLVESGGGLVOPGSGRLSCATSGFTFSSDFYEMWVRQPPGKRLZWNVAIAASRNKANDYTE 61
Oy 99 YVDSVGRFTISRDNKNSLYLQWNSLRAEDTAVVYCCARDLKKVKS--SSGWFDDPGRGTTY 158
Db 62 YSAVGRFTISRDNKNSLTLYLQWNSLRAEDTAVYICARDY---GSSYWFYDVGAGTTL 118
Oy 159 TVSS 163
Db 119 TVSS 123

RESULT 15
HV3M_HUMAN
ID HV3M_HUMAN STANDARD; PRT; 119 AA.
AC P01774;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75046755; PubMed=4139708;
RA Capra J.D., Kehoe J.M.;
RT "Structure of antibodies with shared idiotypy: the complete sequence
RT of the heavy chain variable regions of two immunoglobulin M
RT anti-gamma globulins."
RL Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02057; M3HUPM.
DR HSSP: P01772; 2F84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; IG-LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT VARIANT 54 54 N->D (PROBABLY DUE TO DEAMINATION
FT DURING ISOLATION).
FT FTID=VAR_003966.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12953 MW; 2E018AF4DCB2610 CRC64;

Query Match 25.5%; Score 418; DB 1; Length 119;
Best Local Similarity 68.9%; Pred. No. 8.3e-24;
Matches 84; Conservative 17; Mismatches 15; Indels 6; Gaps 2;

Oy 41 VOLVESGGGLVOPGSGRLSCAASGFTFSSYVMSWVRQAPGKGLZWNVAIKQDSCSEKYYV 100
Db 2 VOLVESGGGLVOPGSGRLSCAASGFTFSSYVMSWVRQAPGKGLZWNVAIKQDSCSEKYYA 61
Oy 101 DSVKGRFTISRDNKNSLYLQWNSLRAEDTAVVYCCARDLKKVKS--SSGWFDDPGRGTTY 158
Db 62 DSVKGRFTISRDNKNSLTLYLQWNSLQAZBVALYICARD---AGPYVSPYFAHGGTL 117
Oy 159 VT 160
Db 118 VT 119

Search completed: September 22, 2003, 15:13:48
Job time : 11.7293 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 50.9388 Seconds
(without alignments)
1580.572 Million cell updates/sec

Title: US-10-052-798-10
Perfect score: 1642
Sequence: 1 MTMTTPSGAFLEIFNVKK.....HHHGAPQKLISEEDLNGAA 312

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phase:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	913	55.6	298	11 Q9QYF0	Q9qyf0 mus musculu
2	599.5	36.5	241	11 Q921A6	Q921a6 mus musculu
3	552	33.6	107	4 Q9NSD6	Q9nsd6 homo sapien
4	521	31.7	471	4 Q8TC77	Q8tc77 homo sapien
5	500.5	30.5	613	4 Q8WUK1	Q8wuk1 homo sapien
6	496	30.2	218	11 Q925L1	Q925l1 mus musculu
7	495	30.1	95	4 Q9ULB6	Q9ulb6 homo sapien
8	494.5	30.1	113	4 Q9UL90	Q9ul90 homo sapien
9	481	29.3	118	4 Q9UL91	Q9ul91 homo sapien
10	479	29.2	487	11 Q99KA4	Q99ka4 mus musculu
11	476	29.0	597	4 Q96B89	Q96b89 homo sapien
12	468.5	28.5	116	4 Q9UL93	Q9ul93 homo sapien
13	466	28.4	494	4 Q96K68	Q96k68 homo sapien
14	463.5	28.2	499	4 Q8NSK4	Q8nsk4 homo sapien
15	461	28.1	122	4 Q9UL84	Q9ul84 homo sapien
16	459.5	28.0	121	4 Q9UL71	Q9ul71 homo sapien

17	455	27.7	573	4 Q8WU38	Q8wu38 homo sapien
18	452	27.5	147	4 Q9Y509	Q9y509 homo sapien
19	447.5	27.3	479	11 Q91WP5	Q91wp5 mus musculu
20	445.5	27.1	473	11 Q91Z05	Q91z05 mus musculu
21	445	27.1	118	4 Q9UL72	Q9ul72 homo sapien
22	442.5	26.9	486	11 Q91Z07	Q91z07 mus musculu
23	441	26.9	112	4 Q9HC1	Q9hcc1 homo sapien
24	437.5	26.6	119	11 Q920E7	Q920e7 mus musculu
25	435.5	26.5	493	4 Q8NCL6	Q8nc16 homo sapien
26	434	26.4	233	4 Q8TRC9	Q8trc9 homo sapien
27	427.5	26.0	480	11 Q91XEL	Q91xel mus musculu
28	426.5	26.0	131	4 Q9UL88	Q9ul88 homo sapien
29	424.5	25.9	521	4 Q8N4Y9	Q8n4y9 homo sapien
30	421.5	25.7	469	11 Q8R3V9	Q8r3v9 mus musculu
31	418	25.5	233	4 Q8NSF4	Q8nsf4 homo sapien
32	409	24.9	484	11 Q8VEAO	Q8vea0 mus musculu
33	394.5	24.0	437	11 Q9R1A4	Q9r1a4 mus musculu
34	381.5	23.2	234	4 Q8N355	Q8n355 homo sapien
35	371.5	22.6	107	4 Q9UL82	Q9ul82 homo sapien
36	366	22.3	124	6 Q9N0W4	Q9n0w4 oryctolaqus
37	363	22.1	124	6 Q9N0W6	Q9n0w6 oryctolaqus
38	363	22.1	237	4 Q8WUK4	Q8wuk4 homo sapien
39	362	22.0	124	4 Q9UL92	Q9ul92 homo sapien
40	357.5	21.8	104	4 Q9UL87	Q9ul87 homo sapien
41	351.5	21.4	112	4 Q9UGP3	Q9ugp3 homo sapien
42	350	21.3	237	4 Q8WTU6	Q8wtu6 homo sapien
43	346.5	21.1	43	4 Q96E61	Q96e61 homo sapien
44	338.5	20.6	119	4 Q9UL94	Q9ul94 homo sapien
45	338	20.6	159	4 Q96QSO	Q96qso homo sapien

ALIGNMENTS

RESULT 1

Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE CN 8 scfv.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=20183931; PubMed=10706631;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phase display subtraction
RT method.";
RT Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
RU EMBL; AB036341; BAA86633.1; -.
DR HSSP; P01607; IRET.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV_2.
DR PROSITE; PSS0835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F9658A17004317 CRC64;

Query Match 55.6%; Score 913; DB 11; Length 298;
Best Local Similarity 62.8%; Pred. No. 5.9e-63;

Matches 186; Conservative 25; Mismatches 65; Indels 20; Gaps 5;

OY 1 MTMTTPSGAFLEIFNVKKLLFAIPLVVPPYAPAPAMAGVOLVSGGGLVPGGSLRLS 60
DB 1 MTMTTPSGAFLEIFNVKKLLFAIPLVVPPYAPAPAMAGVOLVSGGGLVPGGSLRLS 60

```

OY 61 CAAGFTTSSWYMWVROAPGKLEWVANIKODGSEKYYVDSYKGFRTISRDNKNSLYL 120
DB 61 CAAGSDFSRKYMWSVWROAPGKLEWGEINPDSSRTINTYPSLKDFRTISRDNKNSLYL 120
OY 121 QMNSLRADETAVYICARDLKTKGSSSGFDPWGGTGYTVSSGGSGGGSGGGSSG 179
DB 121 QMSKYRSEDTALYYCAR-----ASYGHSAYWGGQGYTVSSGGSGGGSGGGSDI 174
OY 180 ELTODPA-VSYVALGOTVRITCOGDSLRSYASWYOOKPGQAPVLYIGKNNRPSGIDPRF 238
DB 175 ELTODPASISASVGETVITTCASGNINHYLAWYQOKQKSQLLYVNAKTLADGVPSRF 234
OY 239 GSSSGNTASTLTITGAQAEDEADYYCNSRDSGNN-----VYFGGCTKLTVLGAA 289
DB 235 SSGSGGTQYSLKINSIQEPDFSGSYC-----QHFWTPTPYFGGCTKLKIRAA 283

RESULT 2
OY 0921A6 PRELIMINARY; PRT; 241 AA.
AC 0921A6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scfv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL: U88067; AA848044.1; -
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00406; Igv; 2.
DR PROSITE: PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match 36.5%; Score 599.5; DB 11; Length 241;
Best Local Similarity 51.4%; Pred. No. 9,3e-39;
Matches 128; Conservative 35; Mismatches 65; Indels 21; Gaps 7;

OY 41 VOLVESGGGLVPGGSLRSCAASGTFSSYKMSWROAPGKLEWVANIKODGSKYYV 100
DB 2 VRLQSGPELKRPGETVTKSCASGYTFDYGNMVKQAPGKGLKMGAINITYTGEPYA 61
OY 101 DSVKGFRTISRDNKNSLYLQMNLSRAEDTAVYICAR-DLTKVSGSSGMPDPWGGTIV 159
DB 62 DDFKGFRTISRDNKNSLYLQMNLSRAEDTAVYICAR-DLTKVSGSSGMPDPWGGTIV 114
OY 160 TVSSGGSGGGSGGGSSGSS-ELTODP-AVSVALGOTVRITCOGDSLRSYASWYOOKPG 217
DB 115 TVSSGGSGGGSGGGSDIELTQSPSLASLSLGKVTITTCASQDINKYIATWYQHRG 174
OY 218 QAP-----VLYIGKNNRPSGIDPRSGSSSGNTASTLTITGAQAEDEADYYCNSRDSGNN 273
DB 175 KQPRSAHTLHYIQ-----PGIPRSFGSSGSDRYSFISNLBEDIATYYCLAHYD---NL 227
OY 274 VYFGGCTKL 282
DB 228 HTFGGCTKL 236

```

```

RESULT 3
OY 09NSD6 PRELIMINARY; PRT; 107 AA.
AC 09NSD6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-Lymphocytes;
RA Hohmann A.;
RT "Autoimmunity.";
RT Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RL EMBL: I43092; AAA69746.2; -.
DR HSP: P01709; 2MCG.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; Igv; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 33.6%; Score 552; DB 4; Length 107;
Best Local Similarity 98.1%; Pred. No. 1.6e-35;
Matches 105; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 180 ELTODPASVVALGOTVRITCOGDSLRSYASWYOOKPGQAPVLYIGKNNRPSGIDPRF 239
DB 1 ELTODPVSYVALGOTVRITCOGDSLRSYASWYOOKPGQAPVLYIGKNNRPSGIDPRF 60
OY 240 GSSSGNTASTLTITGAQAEDEADYYCNSRDSGNNHVFGGCTKLTVLG 286
DB 61 GSSSGNTASTLTITGAQAEDEADYYCNSRDSGNNHVFGGCTKLTVLG 107

RESULT 4
OY 08TC77 PRELIMINARY; PRT; 471 AA.
AC 08TC77;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-Spleen;
RA Strausberg R.;
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC024289; AA824289.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00406; Igv; 1.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7FACF588660E CRC64;

```

```
Query Match          31.7%; Score 521; DB 4; Length 471;
Best Local Similarity 50.2%; Pred. No. 2.7e-32;
Matches 118; Conservative 22; Mismatches 69; Indels 26; Gaps 5;

QY 41 VOLVSSGGGLVOPGSLRLSCAASGFTSSYMWNVROAPGKGLWMVANIKODGSEKYYV 100
   |||||
DB 21 VOLVSSGGGLVOPGSLRLSCAASGFTSSYMNVRQAPGKGLWMVSMSSSSYIYYA 80
   |||||
QY 101 DSVKGRFTISRDNANKNSLYLQMNSLRAEDTAVYYCARDLKVKSSSGWFDPWGRTYT 160
   |||||
DB 81 DSVKGRFTISRDNANKNSLYLQMNSLRAEDTAVYYCARDLRLQ--TSYTFDLMGSTLYT 138
   |||||
QY 161 VSSGGGGSGGGGSGGSSSELTQDPAYVALGQTVRTTCQGDLSLRSYYASWYQKPGQAP 220
   |||||
DB 139 VSS-----ASTKGPVSFPLAPSSKSTSGCTAALGC--LVKDYFPE-----P 177
   |||||
QY 221 VLVIYGNKNNRPSGI---PDRFSGSSSGMTASLTITGAQAEDEADYVCSRDSSGN 272
   |||||
DB 178 VTVSNVSGALTSRGVHTFPFAVLQSSGLYSLSVYTVVSSSLGTQTYICNVNKRPSN 232
   |||||

RESULT 5
Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC 08WUK1;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Tonsil;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match          30.5%; Score 500.5; DB 4; Length 613;
Best Local Similarity 48.0%; Pred. No. 1.5e-30;
Matches 120; Conservative 14; Mismatches 63; Indels 53; Gaps 8;

QY 41 VOLVSSGGGLVOPGSLRLSCAASGFTSSYMWNVROAPGKGLWMVANIKODGSEKYYV 100
   |||||
DB 21 VOLVSSGGGLVOPGSLRLSCAASGFTSSYGMHVRQAPGKGLWMVAIVSYDGSNKYYA 80
   |||||
QY 101 DSVKGRFTISRDNANKNSLYLQMNSLRAEDTAVYYCARDLKVKSSSGW-----FDPWG 154
   |||||
DB 81 DSVKGRFTISRDNANKNSLYLQMNSLRAEDTAVYYCAKD-----WSEGEVFDTWG 130
   |||||
QY 155 RGTIVTVSSGGGSGGGGSSSELTQDPAYVALG---QTVRTTCQGDSTL--RSY 208
   |||||
DB 131 QGTIVTVSS-----GSASAPTLFPLVSCSENPSPDSSVAVAGCLADFLPDSIT 178
   |||||
QY 209 ASWYQKPGQAPVLYIYGNKNN---RPSGIDPFRFSGSSSGMTASLTITGAQAEDEADYV- 263
   |||||
DB 179 FSWKY-----KNSDISSTRGFPVLRGKRYAATSQVLLPDKVMQGTDEHY 225
   |||||
QY 264 -CNSRDSSGN 272
   |||||
DB 226 VCKVQHPNGN 235
   |||||
```

```
RESULT 6
Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c;
RX Pubmed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RT World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RT Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;
```

```
Query Match          30.2%; Score 496; DB 11; Length 218;
Best Local Similarity 46.4%; Pred. No. 8.7e-31;
Matches 102; Conservative 38; Mismatches 68; Indels 12; Gaps 4;

QY 38 MAGVOLVSSGGGLVOPGSLRLSCAASGFTSSYMWNVROAPGKGLWMVANIKODGSEK 97
   |||||
DB 1 MAQVQLQSGPELTKPGETVTRISCAASGYFTTACGMQWVQKPKGKLGWIGINTHSGVP 60
   |||||
QY 98 YVDSVKGRTISRDNANKNSLYLQMNSLRAEDTAVYYCARDLKVKSSSGWFDPWGRT 157
   |||||
DB 61 KYAEFKGRFPAFSLSTASATVLAQISNLKNEDTATVFCMR-----WDYDGFAYWGGT 114
   |||||
QY 158 TVTVSSGGGSGGGGSGGSS-ELTQDPA-VSVALGQTVRTTCG----DSLRSYVSW 211
   |||||
DB 115 TVTVSSGGGSGGGGSGGSDIVLTQSPASIAVSLGORATISCRASESVNIGISFMNW 174
   |||||
QY 212 YQKPGQAPVLYIYGNKNNRPSGIDPFRFSGSSSGMTASLTIT 251
   |||||
DB 175 FQKPGQPPKLLITVAASKQSGVPAGLLASGSGTDFSLNT 214
   |||||
```

```
RESULT 7
Q9ULB6 PRELIMINARY; PRT; 95 AA.
AC Q9ULB6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Immunoglobulin heavy chain (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence.";
RL Submitted (NOV-1999) to the EMBL/Genbank/DDJ databases.
DR EMBL: AB035268; BAA87067.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match
Best Local Similarity 30.1%; Score 495; DB 4; Length 95;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 VOLVESGGGLVPGGSLRLSCAASGFTSSYMSWVRQAPGKGLEWVANIKDGSSEKYYV 100
DB 1 VOLVESGGGLVPGGSLRLSCAASGFTSSYMSWVRQAPGKGLEWVANIKDGSSEKYYV 60
QY 101 DSVKGRFTISRDNKNSLYLQNSLRRAEDTAVYYC 135
DB 61 DSVKGRFTISRDNKNSLYLQNSLRRAEDTAVYYC 95

RESULT 8
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035024; AAD56260.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match
Best Local Similarity 30.1%; Score 494.5; DB 4; Length 113;
Matches 97; Conservative 7; Mismatches 8; Indels 11; Gaps 1;

QY 41 VOLVESGGGLVPGGSLRLSCAASGFTSSYMSWVRQAPGKGLEWVANIKDGSSEKYYV 100
DB 2 VOLVESGGGLVPGGSLRLSCAASGFTSSYMSWVRQAPGKGLEWVANIRYDGSNKYYA 61
QY 101 DSVKGRFTISRDNKNSLYLQNSLRRAEDTAVYYCARDLLKVGSSSGMFDWGRGITYT 160
```

```
DB 62 DSVKGRFTISRDNKNSLYLQNSLRRAEDTAVYYCAKDL-----NWGGGLVY 110
QY 161 VSS 163
DB 111 VSS 113

RESULT 9
Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035023; AAD56259.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match
Best Local Similarity 29.3%; Score 481; DB 4; Length 118;
Matches 98; Conservative 3; Mismatches 15; Indels 6; Gaps 1;

QY 41 VOLVESGGGLVPGGSLRLSCAASGFTSSYMSWVRQAPGKGLEWVANIKDGSSEKYYV 100
DB 2 VOLVESGGGLVPGGSLRLSCAASGFTSSYMSWVRQAPGKGLEWVSYISTITITYA 61
QY 101 DSVKGRFTISRDNKNSLYLQNSLRRAEDTAVYYCARDLLKVGSSSGMFDWGRGITYT 160
DB 62 DSVKGRFTISRDNKNSLYLQNSLRRAEDTAVYYCAR-----GDSSEAFDWMGGTWT 115
QY 161 VS 162
DB 116 VS 117

RESULT 10
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 52.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagaitsuna M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto Y., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NEO human cDNA sequencing project."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK027379; BAB55072.1; -
 DR InterPro: IPR007110; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_4.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein
 SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AE5AE64C0E CRC64;

Query Match 28.4%; Score 466; DB 4; Length 494;
 Best Local Similarity 74.8%; Pred. No. 5.3e-28;
 Matches 92; Conservative 9; Mismatches 20; Indels 2; Gaps 1;

OY 41 VOLVESGGGLVPGGSLRLSCAASGFTSSYWMVNRQAPGKGLEWVANIKDGSSEKYYV 100
 |||||
 DB 21 VOLVESGGGLVPGGSLRLSCAASGFTSSYWMVNRQAPGKGLEWVSSISRSYIYR 80
 |||||
 OY 101 DSVKGRFTISRDNANKNSLYLNMRARDEYAYVCARDLKYKSSSGWFDPMGRTYV 160
 |||||
 DB 81 DSVKGRFTISRDNANKNSLYLNMRARDEYAYVCARDLKYKSSSGWFDPMGRTYV 138
 |||||
 OY 161 VSS 163
 |||||
 DB 139 VSS 141
 |||||
 RESULT 14
 O8N5K4 PRELIMINARY; PRT; 499 AA.
 AC O8N5K4;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC032249; AAH32249.1; -
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig_Like.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_4.
 DR SMART; SM00409; Ig; 4.
 DR SMART; SM00407; IGc1; 2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.

SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;
 Query Match 28.2%; Score 463.5; DB 4; Length 499;
 Best Local Similarity 73.8%; Pred. No. 8.4e-28;
 Matches 93; Conservative 9; Mismatches 21; Indels 3; Gaps 2;

OY 41 VOLVESGGGLVPGGSLRLSCAASGFTSSYWMVNRQAPGKGLEWVANIKDGSSEKYYV 100
 |||||
 DB 21 VOLVESGGGLVPGGSLRLSCAASGFTSSYWMVNRQAPGKGLEWVSSISRSYIYR 80
 |||||
 OY 101 DSVKGRFTISRDNANKNSLYLNMRARDEYAYVCARDLKYKSSSGWFDPMGRTYV 157
 |||||
 DB 81 DSVKGRFTISRDNANKNSLYLNMRARDEYAYVCARDLKYKSSSGWFDPMGRTYV 140
 |||||
 OY 158 TVTVSS 163
 |||||
 DB 141 TVTVSS 146
 |||||

RESULT 15
 O9UL84 PRELIMINARY; PRT; 122 AA.
 ID O9UL84;
 AC O9UL84;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035030; AAD56266.1; -
 DR HSP; P01772; 2F84.
 DR InterPro: IPR007110; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 122
 FT NON_TER 122
 SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 28.1%; Score 461; DB 4; Length 122;
 Best Local Similarity 75.0%; Pred. No. 2.1e-28;
 Matches 93; Conservative 9; Mismatches 18; Indels 4; Gaps 2;

OY 41 VOLVESGGGLVPGGSLRLSCAASGFTSSYWMVNRQAPGKGLEWVANIKDGSSEKYYV 100
 |||||
 DB 2 VOLVESGGGLVPGGSLRLSCAASGFTSSYWMVNRQAPGKGLEWVAISNDGSNKRYA 61
 |||||
 OY 101 DSVKGRFTISRDNANKNSLYLNMRARDEYAYVCARDLKYKSSSGWFDPMGRTYV 159
 |||||
 DB 62 DSVKGRFTISRDNANKNSLYLNMRARDEYAYVCARDLKYKSSSGWFDPMGRTYV 118
 |||||
 OY 160 TVSS 163
 |||||
 DB 119 TVSS 122
 |||||

Search completed: September 22, 2003, 15:21:24
 Job time : 51.938 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 51.9441 Seconds
(without alignments)
947.272 Million cell updates/sec

Title: US-10-052-798-11
Perfect score: 1638
Sequence: 1 MTMTIPSGCAFFLEIFNVK.....HHGAAEQKLISEEDLNGAA 310

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq.19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1638	100.0	310	20	AAW83324
2	1638	100.0	310	23	ABB09605
3	1638	100.0	310	24	ABG74386
4	1231.5	75.2	309	20	AAW83322
5	1231.5	75.2	309	23	ABB09603
6	1231.5	75.2	309	24	ABG74384
7	1231	75.2	312	23	AAW83323
8	1231	75.2	312	23	ABB09604
9	1231	75.2	312	24	ABG74385

10	1108.5	67.7	252	23	ABP45508	Human Blys binding
11	1089.5	66.5	252	23	ABP44970	Human Blys binding
12	1087.5	66.4	252	23	ABP45197	Human Blys binding
13	1075.5	65.7	246	21	AAV58235	Internalising anti
14	1071	65.4	243	23	ABP45938	Human Blys binding
15	1064.5	65.0	248	23	ABP45879	Human Blys binding
16	1063	64.9	247	23	ABP45942	Human Blys binding
17	1053.5	64.3	258	23	ABP45830	Human Blys binding
18	1050.5	64.1	256	23	ABP45447	Human Blys binding
19	1048.5	64.0	256	23	ABP44828	Human Blys binding
20	1046.5	63.9	250	23	ABP45450	Human Blys binding
21	1045.5	63.8	252	23	ABP45351	Human Blys binding
22	1045.5	63.8	254	23	ABP44970	Human Blys binding
23	1035.5	63.2	250	23	ABP45409	Human Blys binding
24	1033	63.1	304	22	AA65634	Amino acid sequenc
25	1031	62.9	251	23	ABP45298	Human Blys binding
26	1030.5	62.9	252	23	ABP45616	Human Blys binding
27	1028.5	62.8	614	23	ABB06275	Plasmid scfv(C046
28	1027.5	62.7	254	23	ABP44972	Human Blys binding
29	1027	62.7	247	23	ABP46081	Human Blys binding
30	1027	62.7	251	23	ABP45531	Human Blys binding
31	1027	62.7	304	22	AA65639	Amino acid sequenc
32	1026	62.6	251	23	ABP45400	Human Blys binding
33	1024	62.5	253	23	ABP44847	Human Blys binding
34	1023.5	62.5	254	23	ABP45748	Human Blys binding
35	1023	62.5	251	23	ABP44944	Human Blys binding
36	1021.5	62.4	254	23	ABP44870	Human Blys binding
37	1021	62.3	247	23	ABP45881	Human Blys binding
38	1021	62.3	247	23	ABP45967	Human Blys binding
39	1020	62.3	251	23	ABP45321	Human Blys binding
40	1018	62.1	246	23	ABP45945	Human Blys binding
41	1017.5	62.1	249	24	ABJ19834	Human VEGF-2 relat
42	1016	62.0	253	23	ABP45189	Human Blys binding
43	1015.5	62.0	253	22	ABP45603	Huntlingtin Intrabo
44	1015.5	62.0	252	23	ABP44945	Human Blys binding
45	1013	61.8	253	24	ABJ19830	Human VEGF-2 relat

ALIGNMENTS

RESULT 1
AAW83324
ID AAW83324 strand: Protein: 310 AA.
XX
AC AAW83324:
XX
DT 16-MAR-1999 (first entry)
XX
DE Single chain Apo-2 antibody 24C4.
XX
KW Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
KW TNF cytokine.
XX
OS Homo sapiens.
XX
PN WO9851793-A1.
XX
PD 19-NOV-1998.
XX
PF 14-MAY-1998; 98WO-US09704.
XX
PR 09-FEB-1998; 98US-0020746.
XX
PR 15-MAY-1997; 97US-0857216.
XX
PA (GETH) GENENTECH INC.
XX
PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
DR WPI: 1999-045228/04.
XX N-PSDB: AAV72534.
XX

PT Human Apo-2 polypeptide inducing apoptosis - useful to treat
 PT conditions linked with decreased apoptosis e.g. cancer, and produce
 PT antibodies to increase or decrease apoptosis

XX Example 14; Fig 16; 134pp; English.

CC The present invention describes human Apo-2. Apo-2 can be used
 CC therapeutically to induce apoptosis in mammalian cells, and so is useful
 CC to treat conditions associated with decreased apoptosis e.g. cancer.
 CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor
 CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by
 CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It
 CC can be used to identify agents activating Apo-2; useful to treat
 CC mammalian cancer cells, and to produce Apo-2 chimeras useful
 CC therapeutically (e.g. those containing immunoglobulin sequences can be
 CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
 CC tag polypeptide allow Apo-2 detection and purification using anti-tag
 CC antibodies). It can be used to produce antibodies which can be combined
 CC with a (particularly pharmaceutically acceptable) carrier in compositions
 CC or used to produce dimeric molecules (especially homodimeric molecules
 CC comprising first and second Apo-2 antibodies). Agonistic (especially
 CC single-chain) antibodies can be administered to induce apoptosis in
 CC mammalian cancer cells, and antagonistic antibodies used to block
 CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
 CC antibodies may also be used diagnostically e.g. to detect Apo-2
 CC expression in cells/tissues and in Apo-2 purification. The present
 CC sequence represents a single chain Apo-2 antibody, designated 24c4.

XX Sequence 310 AA:

Query Match 100.0%; Score 1638; DB 20; Length 310;

Best Local Similarity 100.0%; Pred. No. 3.7e-103;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTMTIPSCAFLEIFNFKLLFAIPLVVFFYAAPAMAOVOLVOSGGGVOPGRSLRLS 60
 DB 1 MTMTIPSCAFLEIFNFKLLFAIPLVVFFYAAPAMAOVOLVOSGGGVOPGRSLRLS 60
 QY 61 CAASGFIFSSYGMHWRQAPRGKLEWVAGIFYDGNKYYADSVKGRFTISRDNKNTLYL 120
 DB 61 CAASGFIFSSYGMHWRQAPRGKLEWVAGIFYDGNKYYADSVKGRFTISRDNKNTLYL 120
 QY 121 QNNSLRAEEDTAVYYCARDRGYYMDVWGKTTVTYVSSGGGSGGGGSGQSIVLTQPP 180
 DB 121 QNNSLRAEEDTAVYYCARDRGYYMDVWGKTTVTYVSSGGGSGGGGSGQSIVLTQPP 180
 QY 181 SVSGAPGQRVTISCTGRSSNIGAGHDVHYQQLPGTAPKLLTYDSSNRPSSGVPDRFSSGR 240
 DB 181 SVSGAPGQRVTISCTGRSSNIGAGHDVHYQQLPGTAPKLLTYDSSNRPSSGVPDRFSSGR 240
 QY 241 SGTASLAITGLQAEDEADYQCQSYDSSLRGSVFGGTRKVTYVLAAGAAHHHHHGAAEQKL 300
 DB 241 SGTASLAITGLQAEDEADYQCQSYDSSLRGSVFGGTRKVTYVLAAGAAHHHHHGAAEQKL 300
 QY 301 ISEEDLNGAA 310
 DB 301 ISEEDLNGAA 310

RESULT 2
 ABB09605
 ID ABB09605 standard; Protein; 310 AA.

XX ABB09605;

DT 29-MAY-2002 (first entry)

XX Amino acid sequence of single-chain Apo-2 antibody 24c4.

XX Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;
 KM caspase; apoptosis; cancer; antibody.

XX Bacteriophage.

XX US6342369-B1.
 PN 29-JAN-2002.
 PD 14-MAY-1998; 98US-0079029.

XX 15-MAY-1997; 97US-046615P.
 PR 09-FEB-1998; 98US-074119P.

XX (GENTECH) GENENTECH INC.

XX Ashkenazi AJ;

XX WPI; 2002-224941/28.

DR N-PSDB; ABL41735.

PT New nucleic acids encoding an Apo-2 ligand, useful for activating or
 PT stimulating apoptosis in cancer cells, thus especially useful in the
 PT treatment of cancer, or in enhancing immune-mediated cell death

XX Example 14; Fig 16; 63pp; English.

CC The present sequence represents a single-chain Apo-2 antibody, designated
 CC 24c4, which is isolated from a phage library. It is believed that
 CC Apo-2 is a member of the tumour necrosis factor receptor (TNFR)
 CC family. Apo-2 polypeptide is capable of triggering caspase-dependent
 CC apoptosis and activating nuclear factor-kappa B. A soluble
 CC extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2
 CC antibodies may be used to activate or stimulate apoptosis in cancer
 CC cells. They are therefore especially useful in the treatment of cancer,
 CC to enhance immune-mediated cell death in cells expressing Apo-2, to
 CC detect expression of Apo-2 in specific cells, tissues or serum, and in
 CC affinity purification of Apo-2 from recombinant cell culture or natural
 CC sources.

XX Sequence 310 AA:

Query Match 100.0%; Score 1638; DB 23; Length 310;

Best Local Similarity 100.0%; Pred. No. 3.7e-103;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTMTIPSCAFLEIFNFKLLFAIPLVVFFYAAPAMAOVOLVOSGGGVOPGRSLRLS 60
 DB 1 MTMTIPSCAFLEIFNFKLLFAIPLVVFFYAAPAMAOVOLVOSGGGVOPGRSLRLS 60
 QY 61 CAASGFIFSSYGMHWRQAPRGKLEWVAGIFYDGNKYYADSVKGRFTISRDNKNTLYL 120
 DB 61 CAASGFIFSSYGMHWRQAPRGKLEWVAGIFYDGNKYYADSVKGRFTISRDNKNTLYL 120
 QY 121 QNNSLRAEEDTAVYYCARDRGYYMDVWGKTTVTYVSSGGGSGGGGSGQSIVLTQPP 180
 DB 121 QNNSLRAEEDTAVYYCARDRGYYMDVWGKTTVTYVSSGGGSGGGGSGQSIVLTQPP 180
 QY 181 SVSGAPGQRVTISCTGRSSNIGAGHDVHYQQLPGTAPKLLTYDSSNRPSSGVPDRFSSGR 240
 DB 181 SVSGAPGQRVTISCTGRSSNIGAGHDVHYQQLPGTAPKLLTYDSSNRPSSGVPDRFSSGR 240
 QY 241 SGTASLAITGLQAEDEADYQCQSYDSSLRGSVFGGTRKVTYVLAAGAAHHHHHGAAEQKL 300
 DB 241 SGTASLAITGLQAEDEADYQCQSYDSSLRGSVFGGTRKVTYVLAAGAAHHHHHGAAEQKL 300
 QY 301 ISEEDLNGAA 310
 DB 301 ISEEDLNGAA 310

RESULT 3
 ABB74386
 ID ABB74386 standard; Protein; 310 AA.

XX ABB74386;

DT 11-APR-2003 (first entry)
 XX Single chain antibody (scfv) fragment 24C4.
 DE
 XX
 KW Apo-2; tumour necrosis factor family; TNFR; gene therapy;
 KW apoptosis; tissue-specific typing; affinity purification;
 KW competitive-type receptor binding assay; mouse; 24C4.
 XX
 OS Mus sp.
 XX
 PN US2002150985-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 02-NOV-2001; 2001US-0052798.
 XX
 PR 15-MAY-1997; 97US-046615P.
 PR 09-FEB-1998; 98US-074119P.
 PR 14-MAY-1998; 98US-0079029.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
 XX WPI; 2003-198287/19.
 DR N-PSDB; ABX16409.
 XX
 PT New Apo-2 polypeptides and polynucleotides, useful for inducing
 PT apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in
 PT quantitative diagnostic assays, or in generating antibodies against
 PT Apo-2 -
 XX
 PS Example 14; Fig 16; 64pp; English.
 XX
 CC The invention describes a novel isolated Apo-2 polypeptide. The Apo-2
 CC polypeptide is useful for inducing apoptosis in mammalian cells, in vivo
 CC or ex vivo gene therapy, in quantitative diagnostic assays, as a control
 CC against samples containing unknown quantities of Apo-2, in generating
 CC antibodies, in affinity purification techniques, and in competitive-type
 CC receptor binding assays when labeled with, for instance, radiolodine,
 CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a
 CC diagnostic for tissue-specific typing. This is the amino acid sequence
 CC of the single chain antibody fragment (svfv) 24C4 used in the
 CC preparation of anti-apo-2 antibodies.
 CC
 XX Sequence 310 AA;
 SO
 Query Match 100.0%; Score 1638; DB 24; Length 310;
 Best Local Similarity 100.0%; Pred. No. 3,7e-103;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 301 ISEEDLNGAA 310
 RESULT 4
 AAW83322
 ID AAW83322 standard; Protein; 309 AA.
 XX
 AC AAW83322;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Single chain Apo-2 antibody 16E2.
 XX
 KW Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
 KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
 KW TNF cytokine.
 XX
 OS Homo sapiens.
 XX
 PN M09851793-A1.
 XX
 PD 19-NOV-1998.
 XX
 PF 14-MAY-1998; 98WO-US09704.
 XX
 PR 09-FEB-1998; 98US-0020746.
 PR 15-MAY-1997; 97US-0857216.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
 XX WPI; 1999-045228/04.
 DR N-PSDB; AAV72532.
 XX
 PT Human Apo-2 polypeptide inducing apoptosis - useful to treat
 PT conditions linked with decreased apoptosis e.g. cancer, and produce
 PT antibodies to increase or decrease apoptosis
 XX
 PS Example 14; Fig 16; 134pp; English.
 XX
 CC The present invention describes human Apo-2. Apo-2 can be used
 CC therapeutically to induce apoptosis in mammalian cells, and so is useful
 CC to treat conditions associated with decreased apoptosis e.g. cancer.
 CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor
 CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by
 CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It
 CC can be used to identify agents activating Apo-2, useful to treat
 CC mammalian cancer cells, and to produce Apo-2 chimeras useful
 CC therapeutically (e.g. those containing immunoglobulin sequences can be
 CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
 CC tag polypeptide allow Apo-2 detection and purification using anti-tag
 CC antibodies). It can be used to produce antibodies which can be combined
 CC with a (particularly pharmaceutically acceptable) carrier in compositions
 CC or used to produce dimeric molecules (especially homodimeric molecules
 CC comprising first and second Apo-2 antibodies). Agonistic (especially
 CC single-chain) antibodies can be administered to induce apoptosis in
 CC mammalian cancer cells, and antagonistic antibodies used to block
 CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
 CC antibodies may also be used diagnostically e.g. to detect Apo-2
 CC expression in cells/tissues and in Apo-2 purification. The present
 CC sequence represents a single chain Apo-2 antibody, designated 16E2.
 CC
 XX Sequence 309 AA;
 SO
 Query Match 75.2%; Score 1231.5; DB 20; Length 309;
 Best Local Similarity 78.0%; Pred. No. 1.1e-75;
 Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

CC antibodies, in affinity purification techniques, and in competitive-type
 CC receptor binding assays when labelled with, for instance, radioiodine,
 CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a
 CC diagnostic for tissue-specific typing. This is the amino acid sequence
 CC of the single chain antibody fragment (scFv) 10E2 used in the
 CC preparation of anti-apo-2 antibodies.

XX Sequence 309 AA;

Query Match 75.2%; Score 1231.5; DB 24; Length 309;
 Best Local Similarity 78.0%; Pred. No. 1.1e-75;
 Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

OY 1 MTMTTPSGAFLEIFNVKLLFAIPLVPPYAAQAPAAQVQVLOSAGGVOPGRSLRLS 60
 DB 1 MTMTTPSGAFLEIFNVKLLFAIPLVPPYAAQAPAAQVQVLOSAGGVOPGRSLRLS 60
 OY 61 CAASGFITSSYGMHNVROAPKGLKLEWVAGITFDGKNKYADSVKGRFTISDNKNTLYL 120
 DB 61 CAASGFITSSYGMHNVROAPKGLKLEWVAGITFDGKNKYADSVKGRFTISDNKNTLYL 120
 OY 61 CAASGFITSSYGMHNVROAPKGLKLEWVAGITFDGKNKYADSVKGRFTISDNKNTLYL 120
 DB 61 CAASGFITSSYGMHNVROAPKGLKLEWVAGITFDGKNKYADSVKGRFTISDNKNTLYL 120
 OY 121 QMNSLRADDTAVVYCAR-----DRGYVMDVMGKGTIVVSSGGSGSGSGSGSSQSVL 176
 DB 121 QMNSLRADDTAVVYCAR-----DRGYVMDVMGKGTIVVSSGGSGSGSGSGSSQSVL 176
 OY 179 TOPPSVSGAPGQRYTISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDSSNRPSGVPDRF 236
 DB 179 TOPPSVSGAPGQRYTISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDSSNRPSGVPDRF 236
 OY 237 SGRSNGTSASLAIITGLQAEDEADYCCSYDSSLRGVSFGGKTIVLGAANHHNHGAA 296
 DB 237 SGRSNGTSASLAIITGLQAEDEADYCCSYDSSLRGVSFGGKTIVLGAANHHNHGAA 296
 OY 297 EOKLISEEDLNGAA 310
 DB 297 EOKLISEEDLNGAA 310
 OY 296 EOKLISEEDLNGAA 309
 DB 296 EOKLISEEDLNGAA 309

RESULT 7

AAW83323
 ID AAW83323 standard; Protein: 312 AA.

AC AAW83323;

DT 16-MAR-1999 (first entry)

DE Single chain Apo-2 antibody 20E6.

KW Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
 KW Tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
 KW TNF cytokine.

XX Homo sapiens.

OS Homo sapiens.

PN WO9851793-A1.

PD 19-NOV-1998.

PF 14-MAY-1998; 98WO-US09704.

PR 09-FEB-1998; 98US-0020746.

PR 15-MAY-1997; 97US-0857216.

PA (GETH) GENENTECH INC.

PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;

DR WPI; 1999-045228/04.

DR N-PSDB; AAV72533.

PT Human Apo-2 polypeptide inducing apoptosis - useful to treat
 PT conditions linked with decreased apoptosis e.g. cancer, and produce
 PT antibodies to increase or decrease apoptosis

XX Example 14; Fig 16; 134pp; English.

PS The present invention describes human Apo-2. Apo-2 can be used
 XX therapeutically to induce apoptosis in mammalian cells, and so is useful
 CC to treat conditions associated with decreased apoptosis e.g. cancer.
 CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor
 CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by
 CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It
 CC can be used to identify agents activating Apo-2, useful to treat
 CC mammalian cancer cells, and to produce Apo-2 chimera useful
 CC therapeutically (e.g. those containing immunoglobulin sequences can be
 CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
 CC tag polypeptide allow Apo-2 detection and purification using anti-tag
 CC antibodies). It can be used to produce antibodies which can be combined
 CC with a (particularly pharmaceutically acceptable) carrier in compositions
 CC or used to produce dimeric molecules (especially homodimeric molecules
 CC comprising first and second Apo-2 antibodies). Agonistic (especially
 CC single-chain) antibodies can be administered to induce apoptosis in
 CC mammalian cancer cells, and antagonistic antibodies used to block
 CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
 CC antibodies may also be used diagnostically e.g. to detect Apo-2
 CC expression in cells/tissues and in Apo-2 purification. The present
 CC sequence represents a single chain Apo-2 antibody, designated 20E6.

SQ Sequence 312 AA;

Query Match 75.2%; Score 1231; DB 20; Length 312;
 Best Local Similarity 77.7%; Pred. No. 1.2e-75;
 Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;

OY 1 MTMTTPSGAFLEIFNVKLLFAIPLVPPYAAQAPAAQVQVLOSAGGVOPGRSLRLS 60
 DB 1 MTMTTPSGAFLEIFNVKLLFAIPLVPPYAAQAPAAQVQVLOSAGGVOPGRSLRLS 60
 OY 61 CAASGFITSSYGMHNVROAPKGLKLEWVAGITFDGKNKYADSVKGRFTISDNKNTLYL 120
 DB 61 CAASGFITSSYGMHNVROAPKGLKLEWVAGITFDGKNKYADSVKGRFTISDNKNTLYL 120
 OY 61 CAASGFITSSYGMHNVROAPKGLKLEWVAGITFDGKNKYADSVKGRFTISDNKNTLYL 120
 DB 61 CAASGFITSSYGMHNVROAPKGLKLEWVAGITFDGKNKYADSVKGRFTISDNKNTLYL 120
 OY 121 QMNSLRADDTAVVYCAR-----DRGYVMDVMGKGTIVVSSGGSGSGSGSGSSQSVL 176
 DB 121 QMNSLRADDTAVVYCAR-----DRGYVMDVMGKGTIVVSSGGSGSGSGSGSSQSVL 176
 OY 173 TOPPSVSGAPGQRYTISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDSSNRPSGVPDRF 232
 DB 173 TOPPSVSGAPGQRYTISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDSSNRPSGVPDRF 232
 OY 237 SGRSNGTSASLAIITGLQAEDEADYCCSYDSSLRGVSFGGKTIVLGAANHHNHGAA 292
 DB 237 SGRSNGTSASLAIITGLQAEDEADYCCSYDSSLRGVSFGGKTIVLGAANHHNHGAA 292
 OY 297 EOKLISEEDLNGAA 310
 DB 297 EOKLISEEDLNGAA 310
 OY 296 EOKLISEEDLNGAA 309
 DB 296 EOKLISEEDLNGAA 309

RESULT 8

ABB09604
 ID ABB09604 standard; Protein: 312 AA.

AC ABB09604;

DT 29-MAY-2002 (first entry)

DE Amino acid sequence of single-chain Apo-2 antibody 20E6.

KW Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;
 KW caspase; apoptosis; cancer; antibody.

OS Bacteriophage.

DR US6342369-B1.

```

PD 29-JAN-2002.
XX
XX 14-MAY-1998; 98US-0079029.
XX
XX 15-MAY-1997; 97US-046615P.
XX
XX 09-FEB-1998; 98US-074119P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ;
XX
XX MPI: 2002-224941/28.
XX
XX N-PSDB; AB141734.
XX
XX New nucleic acids encoding an Apo-2 ligand, useful for activating or
XX stimulating apoptosis in cancer cells, thus especially useful in the
XX treatment of cancer, or in enhancing immune-mediated cell death -
XX
XX Example 14; Fig 16; 68pp; English.
XX
XX The present sequence represents a single-chain Apo-2 antibody, designated
XX CC 20E6, which is isolated from a phage library. It is believed that
XX CC Apo-2 is a member of the tumour necrosis factor receptor (TNFR)
XX CC family. Apo-2 polypeptide is capable of triggering caspase-dependent
XX CC apoptosis and activating nuclear factor-kappa B. A soluble
XX CC extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2
XX CC antibodies may be used to activate or stimulate apoptosis in cancer
XX CC cells. They are therefore especially useful in the treatment of cancer,
XX CC to enhance immune-mediated cell death in cells expressing Apo-2, to
XX CC detect expression of Apo-2 in specific cells, tissues or serum, and in
XX CC affinity purification of Apo-2 from recombinant cell culture or natural
XX CC sources.
XX
XX Sequence 312 AA:
SQ
XX
XX Query Match 75.2%; Score 1231; DB 23; Length 312;
XX Best Local Similarity 77.7%; Pred. No. 1.2e-75;
XX Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;
XX
XX 1 MTMTIPSGAFLEIFNVKLLFAIPLVVFFYAAPAMAOVOLVOSGGGVOPGRLRLS 60
XX 1 MTMTIPSGAFLEIFNVKLLFAIPLVVFFYAAPAMAOVOLVOSGGGVOPGRLRLS 60
XX 1 MTMTIPSGAFLEIFNVKLLFAIPLVVFFYAAPAMAOVOLVOSGGGVOPGRLRLS 60
XX
XX 61 CAASGTFSSYGMHWROAPRGKLEWVAGIFDGGKRYADSVKGRFTISRDNKNTLYL 120
XX 61 CAASGTFSSYGMHWROAPRGKLEWVAGIFDGGKRYADSVKGRFTISRDNKNTLYL 120
XX 61 CAASGTFSSYGMHWROAPRGKLEWVAGIFDGGKRYADSVKGRFTISRDNKNTLYL 120
XX
XX 121 QMNSLRAEDTAYYYCARD-----RgyyMDVMGKTTVYSSGGGGSGGGSGGGGS 172
XX 121 QMNSLRAEDTAYYYCARD-----RgyyMDVMGKTTVYSSGGGGSGGGSGGGGS 172
XX 121 QMNSLRAEDTAYYYCARD-----RgyyMDVMGKTTVYSSGGGGSGGGSGGGGS 172
XX
XX 173 QSVLTQPPSVSGAPGQRTVISTGRRSSNIGAGHDVHWYQQLPCTAPKLLIYDSSNRPSCV 232
XX 173 QSVLTQPPSVSGAPGQRTVISTGRRSSNIGAGHDVHWYQQLPCTAPKLLIYDSSNRPSCV 232
XX 179 -SELTQDPAVSVAGLQTVRITCGDLSL---SYVASWYQOKPGQAPVLYIYKKNRPSGI 234
XX
XX 233 PRFGSGRSGTASLAITGLQADEADYDCOSYDSSLRGVSFGGKRYVTLGAAAHNNH 292
XX 233 PRFGSGRSGTASLAITGLQADEADYDCOSYDSSLRGVSFGGKRYVTLGAAAHNNH 292
XX 235 PDFFSSSSSGNTASLTITGAQADEADYDCNSRDSGNNHVFGGKTKLYLGAHAHHNNH 294
XX
XX 293 HGAAEOKLISEEDLNGAA 310
XX 295 HGAAEOKLISEEDLNGAA 312
XX
XX Db
XX
XX RESULT 9
XX ABG74385
XX ID ABG74385 standard; Protein; 312 AA.
XX
XX AC ABG74385;
XX
XX AC
XX
XX DT 11-APR-2003 (first entry)
XX
XX DE Single chain antibody (scFv) fragment 20E6.

```

```

XX
XX Apo-2; tumour necrosis factor family; TNFR; gene therapy;
XX KM apoptosis; tissue-specific typing; affinity purification;
XX KM competitive-type receptor binding assay; mouse; 20E6.
XX
XX Mus sp.
XX
XX US2002150985-A1.
XX
XX 17-OCT-2002.
XX
XX 02-NOV-2001; 2001US-0052798.
XX
XX PF
XX PR 15-MAY-1997; 97US-046615P.
XX PR 09-FEB-1998; 98US-074119P.
XX PR 14-MAY-1998; 98US-0079029.
XX
XX (GETH ) GENENTECH INC.
XX
XX Adams CW, Ashkenazi AJ, Chuntharapal A, Kim KJ;
XX
XX MPI: 2003-198287/19.
XX
XX N-PSDB; ABX16408.
XX
XX New Apo-2 polypeptides and polynucleotides, useful for inducing
XX PT apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in
XX PT quantitative diagnostic assays, or in generating antibodies against
XX PT Apo-2 -
XX
XX Example 14; Fig 16; 64pp; English.
XX
XX The invention describes a novel isolated Apo-2 polypeptide. The Apo-2
XX CC polypeptide is useful for inducing apoptosis in mammalian cells, in vivo
XX CC or ex vivo gene therapy, in quantitative diagnostic assays, as a control
XX CC against samples containing unknown quantities of Apo-2, in generating
XX CC antibodies, in affinity purification techniques, and in competitive-type
XX CC receptor binding assays when labelled with, for instance, radioiodine,
XX CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a
XX CC diagnostic for tissue-specific typing. This is the amino acid sequence
XX CC of the single chain antibody fragment (scFv) 20E6 used in the
XX CC preparation of anti-apo-2 antibodies.
XX
XX Sequence 312 AA:
SQ
XX
XX Query Match 75.2%; Score 1231; DB 24; Length 312;
XX Best Local Similarity 77.7%; Pred. No. 1.2e-75;
XX Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;
XX
XX 1 MTMTIPSGAFLEIFNVKLLFAIPLVVFFYAAPAMAOVOLVOSGGGVOPGRLRLS 60
XX 1 MTMTIPSGAFLEIFNVKLLFAIPLVVFFYAAPAMAOVOLVOSGGGVOPGRLRLS 60
XX 1 MTMTIPSGAFLEIFNVKLLFAIPLVVFFYAAPAMAOVOLVOSGGGVOPGRLRLS 60
XX
XX 61 CAASGTFSSYGMHWROAPRGKLEWVAGIFDGGKRYADSVKGRFTISRDNKNTLYL 120
XX 61 CAASGTFSSYGMHWROAPRGKLEWVAGIFDGGKRYADSVKGRFTISRDNKNTLYL 120
XX 61 CAASGTFSSYGMHWROAPRGKLEWVAGIFDGGKRYADSVKGRFTISRDNKNTLYL 120
XX
XX 121 QMNSLRAEDTAYYYCARD-----RgyyMDVMGKTTVYSSGGGGSGGGSGGGGS 172
XX 121 QMNSLRAEDTAYYYCARD-----RgyyMDVMGKTTVYSSGGGGSGGGSGGGGS 172
XX 121 QMNSLRAEDTAYYYCARD-----RgyyMDVMGKTTVYSSGGGGSGGGSGGGGS 172
XX
XX 173 QSVLTQPPSVSGAPGQRTVISTGRRSSNIGAGHDVHWYQQLPCTAPKLLIYDSSNRPSCV 232
XX 173 QSVLTQPPSVSGAPGQRTVISTGRRSSNIGAGHDVHWYQQLPCTAPKLLIYDSSNRPSCV 232
XX 179 -SELTQDPAVSVAGLQTVRITCGDLSL---SYVASWYQOKPGQAPVLYIYKKNRPSGI 234
XX
XX 233 PRFGSGRSGTASLAITGLQADEADYDCOSYDSSLRGVSFGGKRYVTLGAAAHNNH 292
XX 233 PRFGSGRSGTASLAITGLQADEADYDCOSYDSSLRGVSFGGKRYVTLGAAAHNNH 292
XX 235 PDFFSSSSSGNTASLTITGAQADEADYDCNSRDSGNNHVFGGKTKLYLGAHAHHNNH 294
XX
XX 293 HGAAEOKLISEEDLNGAA 310
XX 295 HGAAEOKLISEEDLNGAA 312
XX
XX Db

```

RESULT 10
ABP45508
ID ABP45508 standard; Protein: 252 AA.
XX
XX
AC ABP45508;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Bly5 binding scfv SEQ ID 1519.
XX
BLy5: B Lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PE 15-JUN-2001; 2001WO-US91110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
WP1: 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 2215-2216; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Bly5) polypeptides. Bly5 is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Bly5. The antibodies bind to Bly5
CC and so may be used to detect and quantitate the presence of Bly5 in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Bly5. They may also be
CC administered to treat diseases associated with aberrant Bly5 expression
CC and actively such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
XX
SQ Sequence 252 AA;
XX
Query Match 67.7%; Score 1108.5; DB 23; Length 252;
Best Local Similarity 85.3%; Pred. No. 1.9e-67;
Matches 215; Conservative 13; Mismatches 17; Indels 7; Gaps 3
QY 40 QVQLVDSGGGVVQGRSLRLSCAASGFFTFSSYGMHWQAQAPGKGLDWYAGIFYDGANKYY 99
Dy 1 QVQLQESGGGVVQGRSLRLSCAASGFFTFSSYGMHWQAQAPGKGLDWYAVIYDSGSKYY 60
QY 100 ADVQAGKFTTISRDNSKNTLYIQANSLRAEDTAVYIYCADR-----GYR-YMDVWGKTTY 153
|||||
|||||

Db	61	ADSVKGRFTTISHDNSKNTFLYLQMNLSLRAEDTAVVYCAKHQYDILNGYGGFEDYWGQCTMY	120
Oy	154	TVSSGGGSGGGSGGGGGS-QSVLNPQPSGAPGQRYVICTGSRSSNIGAGHDVHWYQD	212
Db	121	TVSSGGGSGGGSGGGGSAQAVLQPPSSVSCAPGQRYVSVCTGSSNIGAGHDVHWYQD	180
Oy	213	LPGTAPKLLIYDSSNRPSGVDPDRFSGSRSGTASLAITGLQAEDEADYVCSQYDSSLRGS	272
Db	181	FPGTAPKLLIYGNRRNSPQVDPDRFSVSKSGTSASLAITGLQAEDEADYVCSQYDSSLRGS	240
Oy	273	VFGGSKTYTVLG	284
Db	241	IFGTGTYTVLG	252
RESULT 11			
ABP44977	ABP44977 standard; Protein; 252 AA.		
XX	AC	ABP44977;	
XX	DT	19-AUG-2002 (first entry)	
XX	DE	Human Blys binding scFv SEQ ID 988.	
XX	KW	Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;	
XX	KW	tumour necrosis factor; B cell proliferation; B cell differentiation;	
XX	KW	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;	
XX	KW	antiaids; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;	
XX	KW	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;	
XX	KW	common variable immunodeficiency; acquired immunodeficiency syndrome.	
OS	Homo sapiens.		
XX	PN	WO200202641-A1.	
XX	PD	10-JAN-2002.	
XX	PF	15-JUN-2001; 2001WO-US19110.	
XX	PR	16-JUN-2000; 2000US-212210P.	
XX	PR	17-OCT-2000; 2000US-240816P.	
XX	PR	16-MAR-2001; 2001US-276248P.	
XX	PR	21-MAR-2001; 2001US-277379P.	
XX	PR	25-MAY-2001; 2001US-293499P.	
PA	(HUKA-) HUMAN GENOME SCI INC.		
PA	(CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.		
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;		
XX	WPI: 2002-114799/15.		
XX	Antibodies against B Lymphocyte Stimulating polypeptides, useful for		
XX	the diagnosis and treatment of cancers and immune disorders -		
XX	Claim 1; Page 1580-1581; 3148pp; English.		
CC	This invention describes novel antibodies that immunospecifically bind to		
CC	B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the		
CC	tumour necrosis factor (TNF) super family and induces B cell		
CC	proliferation and differentiation. The antibodies of the invention have		
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,		
CC	antirheumatic and antiaids activity and can be used in vaccines to		
CC	inhibit the expression and activity of Blys. The antibodies bind to Blys		
CC	and so may be used to detect and quantitate the presence of Blys in		
CC	biological samples and may be used in this way to diagnose disease		
CC	associated with aberrant expression of Blys. They may also be		
CC	administered to treat diseases associated with aberrant Blys expression		
CC	and activity such as cancer, immune, and autoimmune disorders and		
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,		
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and		
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent		

CC the antibodies and fragments of the antibodies described in the method
CC of the invention.

CC Sequence 252 AA;

Query Match 66.5%; Score 1089.5; DB 23; Length 252;

Best Local Similarity 83.4%; Pred. No. 37e-66;

Matches 211; Conservative 14; Mismatches 19; Indels 9; Gaps 3;

40 OVQLVQSGGCVQVQPSRLRLSCAASGFTFSSYGMHWVQAPGKGLWVAGIFYDGKNTY 99

1 EVQLVESGGGVQVQPSRLRLSCAASGFTFSSYGMHWVQAPGKGLWVALLIYDSKITY 60

100 ADVKGRFTTISRDNKNTLYLQMSLRADTAIVYICANDR-----GYMDVWGKGT 152

61 ADVKGRFTTISRDNKNTLYLQMSLRADTAIVYICARSHYDILGLTWYFDLWGRGL 120

153 TVTSSGGGGGGGGGGGGGGSVLTQPPSVGAPGQRTYTICTGRSSNIGAGHDVHWYQ 212

121 TVTSSGGGGGGGGGGGGGGSVLTQPPSVGAPGQRTYTICTGRSSNIGAGHDVHWYQ 179

213 LPTAPKLLIYDDSNRPSGVPDRFSGSRGTSASLAIITGLQAEDEADYCCSYDSSLRGS 272

180 HPGKAPKLMITDYSKRPSGVPDRFSGSRGTSASLAIITGVQAEDEADYCCSYDSSLRGS 239

273 -VFGGGRVTYVLG 284

240 RVFGTGTQYTVLG 252

RESULT 12

ABP45190 standard; Protein: 252 AA.

ABP45190;

19-AUG-2002 (first entry)

Human Blys binding scFv SEQ ID 1201.

Blys: B lymphocyte stimulator; TNF superfamily; human; cytosolic;

tumour necrosis factor; B cell proliferation; B cell differentiation;

immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

common variable immunodeficiency; acquired immunodeficiency syndrome.

Homo sapiens.

WO200202641-A1.

10-JAN-2002.

15-JUN-2001; 2001WO-US19110.

16-JUN-2000; 2000US-212210P.

17-OCT-2000; 2000US-240816P.

16-MAR-2001; 2001US-276248P.

21-MAR-2001; 2001US-277379P.

25-MAY-2001; 2001US-293499P.

(HUMA-) HUMAN GENOME SCI INC.

(CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

WPI: 2002-114799/15.

Antibodies against B Lymphocyte Stimulating polypeptides, useful for

the diagnosis and treatment of cancers and immune disorders -

Claim 1, Page 1835-1836, 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC acquired immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.

CC Sequence 252 AA;

Query Match 66.4%; Score 1087.5; DB 23; Length 252;

Best Local Similarity 84.1%; Pred. No. 5e-66;

Matches 211; Conservative 14; Mismatches 19; Indels 7; Gaps 3;

40 OVQLVQSGGCVQVQPSRLRLSCAASGFTFSSYGMHWVQAPGKGLWVAGIFYDGKNTY 99

1 EVQLVESGGGVQVQPSRLRLSCAASGFTFSSYGMHWVQAPGKGLWVAVSYDGSKITY 60

100 ADVKGRFTTISRDNKNTLYLQMSLRADTAIVYICANDR-----GYMDVWGKGT 153

61 ADVKGRFTTISRDNKNTLYLQMSLRADTAIVYICARSHYDILGLTWYFDLWGRGL 120

154 TVTSSGGGGGGGGGGGGGGSVLTQPPSVGAPGQRTYTICTGRSSNIGAGHDVHWYQ 212

121 TVTSSGGGGGGGGGGGGGGSVLTQPPSVGAPGQRTYTICTGRSSNIGAGHDVHWYQ 180

213 LPTAPKLLIYDDSNRPSGVPDRFSGSRGTSASLAIITGLQAEDEADYCCSYDSSLRGS 272

181 HPGKAPKLMITDYSKRPSGVPDRFSGSRGTSASLAIITGVQAEDEADYCCSYDSSLRGS 240

273 -VFGGGRVTYVLG 283

241 RVFGTGTQYTVLG 251

RESULT 13

AAV58235 standard; Protein: 246 AA.

AAV58235;

27-MAR-2000 (first entry)

Internalising anti-c-erbB-2 receptor antibody scFv f5.

Antibody; c-erbB-2 receptor; marker; cancer; drug targeting;

HER/neu oncogene; tumour-specific; internalisation; non-immunogenic.

Synthetic.

Homo sapiens.

Location/Qualifiers

31..35 "Heavy chain variable region (VH) complementarity

/note= "determining region 1 (CDR1)"

50..66 "VH-CDR2"

/note= "VH-CDR3"

157..170 "Light chain variable region (VL) complementarity

/note= "determining region 1 (CDR1)"

186..192

Region

FT		/note= "VL-CDR2"
FT	Region	225..235
FT		/note= "VL-CDR3"
XX	WO9955367-A1.	
PD	04-NOV-1999.	
XX		
Pf	23-APR-1999;	99WO-USO7395.
XX		
PR	24-APR-1998;	98US-O082953.
XX	12-FEB-1999;	99US-O250056.
PA	(REGC) UNIV CALIFORNIA.	
PI	Marks JD, Foul MA;	
XX		
DR	WPI: 2000-072168/06.	
DR	N-PsDB; AA258235.	
PT		
PS	Novel internalizing antibodies used to treat cancer cells -	
XX	Claim 3; Page 81; 85pp; English.	
CC	This sequence represents an internalising humanised antibody,	
CC	scfv F5, which specifically binds to the extracellular domain	
CC	of the c-erbB-2 receptor, the protein product of the HER/neu oncogene.	
CC	The scfv F5 antibody binds to the epitope of the c-erbB-2 receptor that	
CC	is bound by F5 antibodies. On binding the c-erbB-2 receptor, the	
CC	antibody is transported into the cell. The c-erbB-2 receptor is a marker	
CC	protein which is overexpressed by 30-50% of breast carcinomas and other	
CC	adenocarcinomas, and thus provides a useful cell surface marker for	
CC	specifically targeting tumour cells. The antibodies of the invention	
CC	are used as tumour-targeting molecules for diagnosis and treatment. The	
CC	antibodies can be attached to effector molecules. The effector molecules	
CC	may include cytotoxins such as ricin, abrin or Pseudomonas exotoxin;	
CC	radiolabelled ligands such as growth factors; therapeutic agents such	
CC	as vinblastine, vindesine or melphalan; ribozymes; or antisense	
CC	molecules. The antibodies may also be used for in vivo or in vitro	
CC	detection and/or quantitation of the c-erb-2 receptor and thus diagnosis	
CC	and/or localisation of cancers characterised by expression of c-erb-2.	
CC	Although antibodies have previously been used to target tumour cells,	
CC	their success has been limited. The utility of prior art antibodies has	
CC	been hampered by the paucity of tumour specific antibodies, antibody	
CC	immunogenicity, low binding affinity, and poor tumour penetration.	
CC	Tumour specific human antibodies were available. However, the production	
CC	of human monoclonal antibodies using conventional hybridoma technology	
CC	has proven difficult. Also, most of the antibodies produced react with	
CC	antigens that are also common to non-malignant cells, which makes them	
CC	unsuitable for use as tumour-targeting molecules. The antibodies of the	
CC	invention overcome these difficulties, as they are targeted to a	
CC	tumour-specific antigen, and avoid the problem of immunogenicity as they	
CC	are human in origin.	
XX		
SQ	Sequence 246 AA;	
Qy	Query Match 65.7%; Score 1075.5; DB 21; Length 246;	
	Best Local Similarity 84.6%; Pred. No. 3.2e-65;	
Dd	Matches 208; Conservative 11; Mismatches 26; Indels 1; Gaps	
Db	1 OYOLVOVGSGGVPOGRSLRLSCAASGFFFSSYGMHWVAQGKGLIEWAGIFYDGKNRY 99 1 QVOLVESGGGGLVOPGGSLRLSCAASGFFFRSYAMSWNQADCKGLEWSAISGRDNNYY 60	
Oy	ADSVKGRRFTTISRDKSKNTLYLQNMSLRADPDAVYYCAR-DGGYYYIMDWMGKTYYTVSSG 158 100 ADVSXKRGFRJTISRDKSKNTLYIQNMSTRADPDAVYYCAAMTSNAFAFDYWGCGTLVTYSSG 120 61	
Oy	GGGSGGGGGSQSIVLTQPPSYSGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGTAP 218 121 GGGSGGGGGSQSIVLTQPPSYSGAPGQVTTISCTSSSNIGAGYGVHWYQQLPGTAP 180	

QY	219	KLLIYDDSNRPGVDPDRSGSGSISASLAITGLQAEDEADYYCOSTDSSLKRSVREGGT	278
DB	181	KLIIIGNNRPSGVPDRFGSGFSKGSASLAITGLQAEDEADYYCQFYDSSLGVMFGGCT	240
QY	279	KVTYVG 284	
DB	241	KLTYVG 246	
RESULT 14			
ABP45958			
XX	ABP45958 standard; Protein; 243 AA.		
AC			
XX	ABP45958;		
DT	19-AUG-2002 (first entry)		
DE	Human Blys binding scFv SEQ ID 1969.		
XX			
KM	Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;		
KM	tumour necrosis factor; B cell proliferation; B cell differentiation;		
KM	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;		
KM	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;		
KM	systemic lupus erythematosus; Rheumatoid arthritis; CVID; AIDS;		
KM	common variable immunodeficiency; acquired immunodeficiency syndrome.		
XX			
OS	Homo sapiens.		
XX			
PM	WO200202641-A1.		
PD	10-JAN-2002.		
XX			
PF	15-JUN-2001; 2001WO-US19110.		
XX			
PR	16-JUN-2000; 2000US-212210P.		
PR	17-OCT-2000; 2000US-240816P.		
PR	16-MAR-2001; 2001US-276248P.		
PR	21-MAR-2001; 2001US-277379P.		
XX	25-MAY-2001; 2001US-293499P.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.		
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;		
DR	WPI: 2002-114799/15.		
XX			
XX	Antibodies against B lymphocyte stimulating polypeptides, useful for		
PT	the diagnosis and treatment of cancers and immune disorders -		
XX			
PS	Claim 1; Page 2750-2751; 3148pp; English.		
XX			
CC	This invention describes novel antibodies that immunospecifically bind to		
CC	B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the		
CC	tumour necrosis factor (TNF) super family and induces B cell		
CC	proliferation and differentiation. The antibodies of the invention have		
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,		
CC	antirheumatic and antiAIDS activity and can be used in vaccines to		
CC	inhibit the expression and activity of Blys. The antibodies bind to Blys		
CC	and so may be used to detect and quantitate the presence of Blys in		
CC	biological samples and may be used in this way to diagnose disease		
CC	associated with aberrant expression of Blys. They may also be		
CC	administered to treat diseases associated with aberrant Blys expression		
CC	and activity such as cancer, immune, and autoimmune disorders and		
CC	diseases, e.g. systemic lupus erythematosus, Rheumatoid arthritis,		
CC	Immunodeficiency (e.g. common variable immunodeficiency (CVID)) and		
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent		
CC	the antibodies and fragments of the antibodies described in the method		
XX	of the invention.		
XX			
SO	Sequence 243 AA;		

Query Match 65.4%; Score 1071; DB 23; Length 243;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 18.3136 Seconds
(without alignments)
716.207 Million cell updates/sec

Title: US-10-052-798-11
Perfect score: 1638
Sequence: 1 MTMTIPSGCAFFLEIFNVK.....HHGADEQKISEEDLNCAA 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1638	100.0	310	US-09-079-029-11	Sequence 11, Appl
2	1231.5	75.2	309	US-09-079-029-9	Sequence 9, Appl
3	1231	75.2	312	US-09-079-029-10	Sequence 10, Appl
4	989.5	60.4	334	US-09-646-028-53	Sequence 53, Appl
5	989.5	60.4	339	US-09-646-028-55	Sequence 55, Appl
6	983.5	60.0	348	US-09-646-028-51	Sequence 51, Appl
7	924.5	56.4	280	US-09-184-658-40	Sequence 40, Appl
8	908.5	55.5	284	US-09-260-527-1	Sequence 1, Appl
9	905	55.3	249	US-10-039-785-53	Sequence 76, Appl
10	877	53.5	245	US-08-918-148-76	Sequence 5, Appl
11	849	51.8	258	US-08-665-202-5	Sequence 5, Appl
12	849	51.8	258	US-09-315-574-5	Sequence 5, Appl
13	848.5	51.8	297	US-09-486-814A-2	Sequence 2, Appl
14	839	51.2	255	US-09-553-498-8	Sequence 8, Appl
15	839	51.2	255	US-09-618-869-8	Sequence 8, Appl
16	833.5	50.9	301	US-08-661-052-14	Sequence 14, Appl
17	833.5	50.9	301	US-09-188-082-14	Sequence 14, Appl
18	833.5	50.9	301	US-09-364-088-14	Sequence 14, Appl
19	833.5	50.9	301	US-09-102-716-14	Sequence 14, Appl
20	827.5	50.5	284	US-08-564-164A-2	Sequence 2, Appl
21	825	50.4	244	US-08-918-148-78	Sequence 78, Appl
22	821.5	50.2	244	US-08-918-148-79	Sequence 79, Appl
23	821	50.1	289	US-09-184-658-63	Sequence 63, Appl
24	819.5	50.0	244	US-08-918-148-77	Sequence 77, Appl
25	811	49.5	245	US-08-918-148-75	Sequence 75, Appl
26	803.5	49.1	244	US-10-039-785-44	Sequence 44, Appl
27	800.5	48.9	278	US-09-260-527-3	Sequence 3, Appl

28	797	48.7	281	US-09-025-769B-178	Sequence 178, App
29	791	48.3	282	US-08-860-174A-10	Sequence 10, Appl
30	790.5	48.3	250	US-10-039-785-50	Sequence 50, Appl
31	788	48.1	245	US-10-039-785-42	Sequence 42, Appl
32	788	48.1	245	US-10-039-785-46	Sequence 46, Appl
33	785	47.9	249	US-08-918-148-74	Sequence 74, Appl
34	779.5	47.6	236	US-08-190-159A-65	Sequence 65, Appl
35	779.5	47.6	553	US-08-661-052-16	Sequence 16, Appl
36	779.5	47.6	553	US-09-188-082-16	Sequence 16, Appl
37	779.5	47.6	553	US-09-364-088-16	Sequence 16, Appl
38	779.5	47.6	553	US-09-102-716-16	Sequence 16, Appl
39	777	47.4	245	US-10-039-785-43	Sequence 43, Appl
40	774	47.3	245	US-10-039-785-48	Sequence 48, Appl
41	772	47.1	245	US-10-039-785-49	Sequence 49, Appl
42	769.5	47.0	240	US-08-956-047-25	Sequence 25, Appl
43	766	46.8	245	US-10-039-785-45	Sequence 45, Appl
44	764.5	46.7	267	US-09-485-737B-2	Sequence 2, Appl
45	760.5	46.4	277	US-08-256-790-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-079-029-11
Sequence 11, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuncharapal, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079, 029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maerschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-11
Query Match 100.0%; Score 1638; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.2e-120;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTMTIPSGCAFFLEIFNVKLLFAIPLVVPPFAAQAQVQVQSGGCVVQPGKSLALS 60
DB 1 MTMTIPSGCAFFLEIFNVKLLFAIPLVVPPFAAQAQVQVQSGGCVVQPGKSLALS 60
QY 61 CAASGFIRSSVGMHVQAPGKLEWVAGIFYDGNKRYVADSVKGRFTISRDNKNTLYL 120

Db 61 CAASGTFSSYGMHWROAPGKLEWVAGIFTDGKNKYADSVKGRFTISRDNKNTLYL 120
QY 121 QNNSLRAEDTAVYYCARDRCGYMDYWGKTTVTSSGGSGGSGGSGSOSVLTQPP 180
Db 121 QNNSLRAEDTAVYYCARDRCGYMDYWGKTTVTSSGGSGGSGGSGSOSVLTQPP 180
QY 181 SVSAGPQRYTICTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDSDNRPSPGVDPFRSGSR 240
Db 181 SVSAGPQRYTICTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDSDNRPSPGVDPFRSGSR 240
QY 241 SGTSSALATITGLQAEDEADYCCSYDSLSRGSVFGGTRKVTYLGAAAHNHHGAAEQKL 300
Db 241 SGTSSALATITGLQAEDEADYCCSYDSLSRGSVFGGTRKVTYLGAAAHNHHGAAEQKL 300
QY 301 ISEEDLINGAA 310
Db 301 ISEEDLINGAA 310

RESULT 2
US-09-079-029-9

; Sequence 9, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntarapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-9

Query Match 75.2%; Score 1231.5; DB 4; Length 309;
Best Local Similarity 78.0%; Pred. No. 2.1e-88;
Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

QY 1 MTMTIPSGAFLEIFNNVKKLLFAIPLVVFFYAAPAMAOVLVOSGGGVQPGSRSLRLS 60
Db 1 MTMTIPSGAFLEIFNNVKKLLFAIPLVVFFYAAPAMAOVLVOSGGGVQPGSRSLRLS 60
QY 61 CAASGTFSSYGMHWROAPGKLEWVAGIFTDGKNKYADSVKGRFTISRDNKNTLYL 120
Db 61 CAASGTFPDYGMHWROAPGKLEWVAGIFTDGKNKYADSVKGRFTISRDNKNTLYL 120

QY 121 QNNSLRAEDTAVYYCAR----DRGYTMDYWGKTTVTSSGGSGGSGGSGSOSVLT 176
Db 121 QNNSLRAEDTAVYYCAKILCAGRWYF-DLMGKTTVTSSGGSGGSGGSGS-SEL 178
QY 177 TOPPSVAGPQRYTICTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDSDNRPSPGVDPFR 236
Db 179 TOPPAVSVALGQVTRTCCGDSLR---STYASVYQOKPQAPVLYTGKNNRPSGIPIRFR 235
QY 237 SGTSSALATITGLQAEDEADYCCSYDSLSRGSVFGGTRKVTYLGAAAHNHHGAA 296
Db 236 SGTSSALATITGLQAEDEADYCCSYDSLSRGSVFGGTRKVTYLGAAAHNHHGAA 295
QY 297 EOKLISEEDLINGAA 310
Db 296 EOKLISEEDLINGAA 309

RESULT 3
US-09-079-029-10

; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntarapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-10

Query Match 75.2%; Score 1231; DB 4; Length 312;
Best Local Similarity 77.7%; Pred. No. 2.4e-88;
Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;

QY 1 MTMTIPSGAFLEIFNNVKKLLFAIPLVVFFYAAPAMAOVLVOSGGGVQPGSRSLRLS 60
Db 1 MTMTIPSGAFLEIFNNVKKLLFAIPLVVFFYAAPAMAOVLVOSGGGVQPGSRSLRLS 60
QY 61 CAASGTFSSYGMHWROAPGKLEWVAGIFTDGKNKYADSVKGRFTISRDNKNTLYL 120
Db 61 CAASGTFSSYGMHWROAPGKLEWVAGIFTDGKNKYADSVKGRFTISRDNKNTLYL 120
QY 121 QNNSLRAEDTAVYYCARD-----RGYYTMDYWGKTTVTSSGGSGGSGGSGS 172
Db 121 QNNSLRAEDTAVYYCARDLLKVGSSSGWF--DPMGRGTTVTSSGGSGGSGGSGS 178

```

QY 173 OSVLTQPPSYSGARGVHTISCTGRSSNIGAGHDVWYQOLPGTAPKLLIYDSDNRPSGV 232
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 179 -SELTQDPAYVALGQVYVITCGDSL---SYTASMYQQKPGAPVLVIYIGKNNRSGI 234
QY 233 PDRSGSRGTSASLATGLQADEADYTCOSYDSSLRGSGVGGTGVTVVIGAAHHHHH 292
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 235 PDRSGSSSGNTASLTITGAQADEADYTCNSRDSGNHVYFGGTGLTVLGAHHHHH 294
QY 293 HGAEOKLISEEDNGAA 310
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 295 HGAEOKLISEEDNGAA 312

```

```

RESULT 4
US-09-646-028-53
; Sequence 53, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-53

```

```

Query Match 60.4%; Score 989.5; DB 4; Length 334;
Best Local Similarity 72.5%; Pred. No. 1.6e-69;
Matches 192; Conservative 25; Mismatches 41; Indels 7; Gaps 4;
QY 33 AAOPMAQVOLVOSGGVOPGRSLRLSCAASGFIFSSYGMHWROAPGKLEWVAGIFY 92
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 73 AQAARKLEVOLEGGGLVOSGSLRLSCVAGSLTFSSAITWROAPGKLEWVAGISGF 132
QY 93 DGGKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDR-GYYMDVWGKGT 151
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 133 SGDTYYADSVKGRFSSASRDNSKNTLYLQMNLRPNDFAVYFCANNOTGNCLDNWGCGT 192
QY 152 TVTWSS--GGGGGGGGGGG--GQSIVLTQPPSYSGARGVHTISCTGRSSNIGAGHDVH 208
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 193 LVTYSSRGGGGGGGGGGGSSQSVLTQPPSYSAAPGQVHTISCTGRSSNIGAGDVN 252
QY 209 WYQOLPGTAPKLLIYDSDNRPSGVDRFSGSGTSASLATGLQADEADYTCOSYDSS 268
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 253 WYQKFPETAPKVLIIYNNRRSGVDRFSGSGTSASLATGLQLEDEGTYTCQCNDS 312
QY 269 LRGSVFGGCTKTVVLGAHHHHHHH 293
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 313 LSGWLFGGGTGLTVL---RHNNHHH 334

```

```

RESULT 5
US-09-646-028-55
; Sequence 55, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-55

```

```

; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-55

```

```

Query Match 60.4%; Score 989.5; DB 4; Length 339;
Best Local Similarity 72.5%; Pred. No. 1.6e-69;
Matches 192; Conservative 25; Mismatches 41; Indels 7; Gaps 4;
QY 33 AAOPMAQVOLVOSGGVOPGRSLRLSCAASGFIFSSYGMHWROAPGKLEWVAGIFY 92
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 AQAARKLEVOLEGGGLVOSGSLRLSCVAGSLTFSSAITWROAPGKLEWVAGISGF 137
QY 93 DGGKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDR-GYYMDVWGKGT 151
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 138 SGDTYYADSVKGRFSSASRDNSKNTLYLQMNLRPNDFAVYFCANNOTGNCLDNWGCGT 197
QY 152 TVTWSS--GGGGGGGGGGG--GQSIVLTQPPSYSGARGVHTISCTGRSSNIGAGHDVH 208
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 198 LVTYSSRGGGGGGGGGGGSSQSVLTQPPSYSAAPGQVHTISCTGRSSNIGAGDVN 257
QY 209 WYQOLPGTAPKLLIYDSDNRPSGVDRFSGSGTSASLATGLQADEADYTCOSYDSS 268
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 258 WYQKFPETAPKVLIIYNNRRSGVDRFSGSGTSASLATGLQLEDEGTYTCQCNDS 317
QY 269 LRGSVFGGCTKTVVLGAHHHHHHH 293
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 318 LSGWLFGGGTGLTVL---RHNNHHH 339

```

```

RESULT 6
US-09-646-028-51
; Sequence 51, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-51

```

```

Query Match 60.0%; Score 983.5; DB 4; Length 348;
Best Local Similarity 73.6%; Pred. No. 4.8e-69;
Matches 190; Conservative 25; Mismatches 36; Indels 7; Gaps 4;
QY 40 OVOLVOSGGVOPGRSLRLSCAASGFIFSSYGMHWROAPGKLEWVAGIFYDGGKYY 99
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 94 EVOLLEGGGLVOSGSLRLSCVAGSLTFSSAITWROAPGKLEWVAGISFGDTYY 153
QY 100 ADVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDR-GYYMDVWGKGTVTWSS- 157
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```



```

: GENERAL INFORMATION:
: APPLICANT: Salcedo et al.
: TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
: TITLE OF INVENTION: Receptors
: FILE REFERENCE: p0550
: CURRENT APPLICATION NUMBER: US/10/039,785
: CURRENT FILING DATE: 2002-05-07
: PRIOR APPLICATION NUMBER: 60/369,860
: PRIOR FILING DATE: 2002-04-05
: PRIOR APPLICATION NUMBER: 60/341,237
: PRIOR FILING DATE: 2001-12-20
: PRIOR APPLICATION NUMBER: 60/331,310
: PRIOR FILING DATE: 2001-11-14
: PRIOR APPLICATION NUMBER: 60/331,044
: PRIOR FILING DATE: 2001-11-07
: PRIOR APPLICATION NUMBER: 60/327,364
: PRIOR FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: 60/323,807
: PRIOR FILING DATE: 2001-09-21
: PRIOR APPLICATION NUMBER: 60/309,176
: PRIOR FILING DATE: 2001-08-02
: PRIOR APPLICATION NUMBER: 60/294,981
: PRIOR FILING DATE: 2001-06-04
: PRIOR APPLICATION NUMBER: 60/293,473
: PRIOR FILING DATE: 2001-05-25
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 53
: LENGTH: 249
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: T1006F07 scfv
US-10-039-785-53

```

```

Query Match 55.3%; Score 905; DB 4; Length 249;
Best Local Similarity 71.1%; Pred. No. 4; le-63;
Matches 180; Conservative 24; Mismatches 37; Indels 12; Gaps 5;

QY 40 QVQVLOSQGGVQVQPGSRSLRSCAASGFISSYGMHWVROAPGKLEWVAGIFPDGKRY 99
DB 1 EVQLLESGGGLVPGGSLRLISCAASGTFSSYAMSVROAPGKLEWVSAISGSGSTYY 60
QY 100 ADVSKGFTISRDNKNTLYLQMSLRAEDTAVYYCARDGQY-----YYMDVWGKGT 152
DB 61 ADVSKGFTISRDNKNTLYLQMSLRAEDTAVYYCARDGQY-----YYMDVWGKGT 120
QY 153 VTVSSGGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 211
DB 121 VTVSSGGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 177
QY 212 QLTGTAPKLLIYDSDNRPSGVPPDFSGSRGTSASLAITGLQAEDEADYYICOSTDSSLRG 271
DB 178 QRGQSGSVLVLYDKNRPSGIPERFSGSNGNTATLKISCTQAMDEADYYICLAWDS-AD 236
QY 272 SVFGGKTYTVLG 284
DB 237 WVEGGKTYTVLG 249

```

```

RESULT 10
US-08-918-148-76
: Sequence 76, Application US/08918148A
: Patent No. 6342220
: GENERAL INFORMATION:
: APPLICANT: Adams, Camellia
: APPLICANT: W.
: APPLICANT: Carter, Paul J.
: APPLICANT: Fendley, Brian M.
: APPLICANT: Gurney, Austin L.
: TITLE OF INVENTION: Agonist Antibodies
: FILE REFERENCE: P0979
: CURRENT APPLICATION NUMBER: US/08/918,148A

```

```

: CURRENT FILING DATE: 1997-08-25
: NUMBER OF SEQ ID NOS: 79
: SEQ ID NO 76
: LENGTH: 245
: TYPE: PRT
: ORGANISM: artificial
US-08-918-148-76

Query Match 53.5%; Score 877; DB 4; Length 245;
Best Local Similarity 71.2%; Pred. No. 6; le-61;
Matches 178; Conservative 18; Mismatches 48; Indels 6; Gaps 4;

QY 38 MAQVQLVQSGGVPQPGSRSLRSCAASGFISSYGMHWVROAPGKLEWVAGIFPDGK 97
DB 1 MAEQVLOSQGGVQVQPGGSLSLSCAVSGITRTGMHWVROAPGKLEWVAGISFDGRSE 60
QY 98 YYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDGQYYYMDVWGKGTYYVSS 157
DB 61 YYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDGQSYGMDVWGKGTMYVSS 120
QY 158 GGGSGGGSGGSGGSGSVLQPPS-VSGAPGQRTISCTGRSSNIGAGHDVHWYQQLPCT 216
DB 121 GGGSGGGSGGSGGSDIQMTQPSPTLSASIGDRTYTC--RASE-GLYHWLAWYQKPGK 177
QY 217 APKLLIYDSDNRPSGVPPDFSGSRGTSASLAITGLQAEDEADYYICOSTDSSLRG 276
DB 178 APKLLIYKASSLAGAPSRFSGSGGTDFTLTISLQPDPRATYYCQY--SNRPLTFGG 235
QY 277 GTKVTVLGAA 286
DB 236 GTKLEILRAA 245

```

```

RESULT 11
US-08-665-202-5
: Sequence 5, Application US/08665202
: Patent No. 5977322
: GENERAL INFORMATION:
: APPLICANT: Marks, James D.
: APPLICANT: Schler, Robert
: TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
: TITLE OF INVENTION: Tumor Antigens
: NUMBER OF SEQUENCES: 141
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/665,202
: FILING DATE: 13-JUN-1996
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/000,238
: FILING DATE: 14-JUN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/000,250
: FILING DATE: 15-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Hunter, Tom
: REGISTRATION NUMBER: 38,498
: REFERENCE/DOCKET NUMBER: 02307E-061410
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 5:

```



```

QY 61 CAASGFIFSYGMHVRQAPGKLEWVAGIF-YDGNKYADVSKRFTISRDNKNTLY 119
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 61 CKASGFTGYNMKWKQNSKSLSEWIGYIYPYNGTG-YNOKFKSKAFLEYDKSSSTAY 119
QY 120 LQMNSLRAEDTAVYICADRGYYVDWVGKTTTVSSGGGGGGGGGGGGGQSVLTQ 178
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 120 MQLSLTSEDSAVYYCAR---LGLDYWGQGTTVVSSGGGGGGGGGGGGSDIELTQS 175
QY 179 PPSVGAAPGQRTVITISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDSDNRPSGVPDRFSG 238
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 176 PTMAASRPEKITTCISA-SSSISNT-LHWYQKPGFSPKLLIIRTSNLSAGTPARFSG 233
QY 239 SRSGTSASLAITGLQAEDEADYCCQSYDSLSRGVFGGRTVYLGAA 287
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 234 SGSGTSYSLTIGTMEADVDATYYCQGGSSIPRIFFGAGTKLEIKRAA 282

```

RESULT 14
US-09-553-498-8
Sequence 8, Application US/09553498

Patent No. 6309861

GENERAL INFORMATION:

APPLICANT: Ambrosius, Dorothee

APPLICANT: Rudolph, Rainer

APPLICANT: Schaeffner, Joerg

APPLICANT: Schwarz, Elisabeth

TITLE OF INVENTION: Process for the production of naturally folded and secreted prote

FILE REFERENCE: Case 20379

CURRENT APPLICATION NUMBER: US/09/553.498

CURRENT FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: EP99107412.1

PRIOR FILING DATE: 1999-04-26

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 8

LENGTH: 255

TYPE: PRT

ORGANISM: E. coli

US-09-553-498-8

Query Match

Best Local Similarity 51.2%; Score 839; DB 4; Length 255;

Matches 173; Conservative 30; Mismatches 51; Indels 20; Gaps 5;

```

QY 38 MAOVOLVGGGCVVQPGRSRLRLSCAASGFIFSSYGMHVRQAPGKLEWVAGIFYDGK 97
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 1 MAEVLQESGGGLVQPGSGSRKLSCAASGFTFSSFGMHVRQAPGKLEWVATISSGSTI 60
QY 98 YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYICARDGYYYMDWVGKTTVYSS 157
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 61 YYADVVKGRFTISRDNKNTLYLQMNSLRAEDTAVYICARDGY---WGQGTTVYSS 116
QY 158 GGGGGGGGGGGGQSVLTQPPSV-SGAPGQRTVITISCTGRSSNIGAGHDVHWYQOLPGT 216
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 117 GGGGGGGGGGGGSDIELTQSPALMSASPGKVTMTCSASS---VRYNMWFOOKSGT 172
QY 217 APKLLIYDSDNRPSGVPDRFSGSRGTSASLAITGLQAEDEADYCCQSYDSLSRGVFGG 276
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 173 SPKRWIYDTSKLSSVPAFSGSGSTSYSLTSSMEADATYYCQGMSSN--PLTFGA 230
QY 277 GTKVTVLGAAAHHHHHGAAEQKLISEEDLNGAA 310
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 231 GTKLELKRA-----AAEQKLISEEDLNGAA 255

```

RESULT 15

US-09-618-869-8

Sequence 8, Application US/09618869

Patent No. 6455279

GENERAL INFORMATION:

APPLICANT: Ambrosius, Dorothee

APPLICANT: Rudolph, Rainer

APPLICANT: Schaeffner, Joerg

APPLICANT: Schwarz, Elisabeth

```

; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND
; TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
; TITLE OF INVENTION: CHAPERONES
; FILE REFERENCE: 20381
; CURRENT APPLICATION NUMBER: US/09/618.869
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: EP99114811.5
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-618-869-8

```

Query Match

Best Local Similarity 51.2%; Score 839; DB 4; Length 255;

Matches 173; Conservative 30; Mismatches 51; Indels 20; Gaps 5;

```

QY 38 MAOVOLVGGGCVVQPGRSRLRLSCAASGFIFSSYGMHVRQAPGKLEWVAGIFYDGK 97
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 1 MAEVLQESGGGLVQPGSGSRKLSCAASGFTFSSFGMHVRQAPGKLEWVATISSGSTI 60
QY 98 YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYICARDGYYYMDWVGKTTVYSS 157
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 61 YYADVVKGRFTISRDNKNTLYLQMNSLRAEDTAVYICARDGY---WGQGTTVYSS 116
QY 158 GGGGGGGGGGGGQSVLTQPPSV-SGAPGQRTVITISCTGRSSNIGAGHDVHWYQOLPGT 216
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 117 GGGGGGGGGGGGSDIELTQSPALMSASPGKVTMTCSASS---VRYNMWFOOKSGT 172
QY 217 APKLLIYDSDNRPSGVPDRFSGSRGTSASLAITGLQAEDEADYCCQSYDSLSRGVFGG 276
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 173 SPKRWIYDTSKLSSVPAFSGSGSTSYSLTSSMEADATYYCQGMSSN--PLTFGA 230
QY 277 GTKVTVLGAAAHHHHHGAAEQKLISEEDLNGAA 310
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 231 GTKLELKRA-----AAEQKLISEEDLNGAA 255

```

Search completed: September 22, 2003, 15:16:02

Job time: 19.3136 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:16:07 : Search time 34.2965 Seconds
(without alignments)
1345.823 Million cell updates/sec

Title: US-10-052-798-11

Perfect score: 1638

Sequence: 1 MTMTTSPGCAFFLEIFNVKK.....HHGAAEQKISEEDLNGAA 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 556269 seqs, 148893369 residues

Total number of hits satisfying chosen parameters: 556269

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PC1_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PC1US_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description
	1	1638	100.0	310	12	US-10-288-917-11	Sequence 11, Appl
	2	1638	100.0	310	14	US-10-052-798-11	Sequence 11, Appl
	3	1231.5	75.2	309	12	US-10-288-917-9	Sequence 9, Appl
	4	1231.5	75.2	309	14	US-10-052-798-9	Sequence 9, Appl
	5	1231	75.2	312	12	US-10-288-917-10	Sequence 10, Appl
	6	1231	75.2	312	14	US-10-052-798-10	Sequence 10, Appl
	7	1108.5	67.7	252	11	US-09-880-748-1519	Sequence 1519, Ap
	8	1089.5	66.4	252	11	US-09-880-748-988	Sequence 988, App
	9	1087.5	66.4	252	11	US-09-880-748-1201	Sequence 1201, Ap
	10	1071	65.4	243	11	US-09-880-748-1969	Sequence 1969, Ap
	11	1064.5	65.0	248	11	US-09-880-748-1890	Sequence 1890, Ap
	12	1063	64.9	247	11	US-09-880-748-1953	Sequence 1953, Ap
	13	1053.5	64.3	258	11	US-09-880-748-1841	Sequence 1841, Ap
	14	1050.5	64.1	260	11	US-09-880-748-1458	Sequence 1458, Ap
	15	1048.5	64.0	256	11	US-09-880-748-839	Sequence 839, App

16	1046.5	63.9	250	11	US-09-880-748-1461	Sequence 1461, Ap
17	1045.5	63.8	252	11	US-09-880-748-1362	Sequence 1362, Ap
18	1045.5	63.8	254	11	US-09-880-748-981	Sequence 981, App
19	1035.5	63.2	250	11	US-09-880-748-1420	Sequence 1420, Ap
20	1031	62.9	251	11	US-09-880-748-1309	Sequence 1309, Ap
21	1030.5	62.9	252	11	US-09-880-748-1627	Sequence 1627, Ap
22	1027.5	62.7	254	11	US-09-880-748-983	Sequence 983, App
23	1027	62.7	247	11	US-09-880-748-2092	Sequence 2092, Ap
24	1027	62.7	251	11	US-09-880-748-1542	Sequence 1542, Ap
25	1026	62.6	251	11	US-09-880-748-1411	Sequence 1411, Ap
26	1024	62.5	253	11	US-09-880-748-858	Sequence 858, App
27	1023.5	62.5	254	11	US-09-880-748-1759	Sequence 1759, App
28	1023	62.5	251	11	US-09-880-748-955	Sequence 955, App
29	1021.5	62.4	254	11	US-09-880-748-881	Sequence 881, App
30	1021	62.3	247	11	US-09-880-748-1892	Sequence 1892, Ap
31	1021	62.3	247	11	US-09-880-748-1978	Sequence 1978, Ap
32	1020	62.3	251	11	US-09-880-748-1332	Sequence 1332, Ap
33	1018	62.1	249	11	US-09-880-748-1956	Sequence 1956, Ap
34	1016	62.0	253	11	US-09-880-748-1200	Sequence 1200, Ap
35	1015.5	62.0	252	11	US-09-880-748-956	Sequence 956, App
36	1012.5	61.8	254	11	US-09-880-748-1139	Sequence 1139, Ap
37	1012	61.8	251	11	US-09-880-748-1317	Sequence 1317, Ap
38	1010.5	61.7	240	11	US-09-880-748-2105	Sequence 2105, Ap
39	1008	61.5	241	11	US-09-880-748-2055	Sequence 2055, Ap
40	1006.5	61.4	240	11	US-09-880-748-1905	Sequence 1905, Ap
41	1005.5	61.4	240	11	US-09-880-748-2007	Sequence 2007, Ap
42	1005.5	61.4	240	11	US-09-880-748-2025	Sequence 2025, Ap
43	1005.5	61.4	240	11	US-09-880-748-2045	Sequence 2045, Ap
44	1004.5	61.3	240	11	US-09-880-748-2016	Sequence 2016, Ap
45	1004.5	61.3	240	11	US-09-880-748-2030	Sequence 2030, Ap

ALIGNMENTS

RESULT 1
US-10-288-917-11
Sequence 11, Application US/10288917
Publication No. US20030148455A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
Ashkenazi, Avi J.
Chuntharapai, Anan
Kim, Kyung J.

TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/288,917
FILING DATE: 06-NOV. US20030148455A1-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/052798
FILING DATE: 02-NOV-2001
APPLICATION NUMBER: 09/079029
FILING DATE: 14-MAY-1998
APPLICATION NUMBER: 60/074119
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 60/046615
FILING DATE: 15-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.

```

      : REGISTRATION NUMBER: 35,600
      : REFERENCE/DOCKET NUMBER: P1101R2D1C1
      : TELECOMMUNICATION INFORMATION:
      :   TELEPHONE: 650/225-9416
      :   TELEFAX: 650/952-9881
      : INFORMATION FOR SEQ ID NO: 11:
      : SEQUENCE CHARACTERISTICS:
      :   LENGTH: 310 amino acids
      :   TYPE: amino acid
      :   TOPOLOGY: Linear
      : US-10-288-917-11
      : SEQUENCE DESCRIPTION: SEQ ID NO: 11:
Query Match          100.0%; Score 1638; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 8,4e-106;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY       1 MTMTTPSGAFLLEFNKLLFAFLPVPEFAAPAMAOVOLVDSGGVGPGRSRLRS 60
Db        1 MTMTTPSGAFLLEFNKLLFAFLPLVPFFFAAPAMAQVOLVDSGGVGPGRSRLRS 60
QY       61 CAASGFITSSGMMHWROAPGKGLEWVAGIFYDGSKNTYYADSVKGRFTISRDNSKNTLYL 120
Db        61 CAASGFITSSGMMHWROAPGKGLEWVAGIFYDGSKNTYYADSVKGRFTISRDNSKNTLYL 120
QY       121 QMNSTLRADPTAVYCARDRGYVMWKGTIVTVSSGGSGSGGSQSGLVLTGP 180
Db        121 QMNSTLRADPTAVYCARDRGYVMWKGTIVTVSSGGSGSGGSQSGLVLTGP 180
QY       181 SVSAGPGRVATISCTGRSSNIGAGHDVHWYOOLPGTAPKLITYDSDNRPSGVPDFRSGSR 240
Db        181 SVSAGPGRVATISCTGRSSNIGAGHDVHWYOOLPGTAPKLITYDSDNRPSGVPDFRSGSR 240
QY       241 SGTSAIAITGLQAEDEADYYCOYSDSLRSVFSGGTRVTVLGAHHHHAAGAEOQL 300
Db        241 SGTSAIAITGLQAEDEADYYCOYSDSLRSVFSGGTRVTVLGAHHHHAAGAEOQL 300
QY       301 ISEEDLNCAA 310
Db        301 ISEEDLNCAA 310

RESULT 2
US-10-052-798-11
Sequence 11, Application US/10052798
Publication No. US20020150985A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
            Ashkenazi, Avi J.
            Chuntcharapai, Anan
            Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin.(Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/052,798
FILING DATE: 02-No. US20020150985A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
```

```

NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-052-798-11

Query Match 100.0%; Score 1638; DB 14; Length 310;
Best Local Similarity 100.0%; Pred. No. 8,4e-106;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Db 1 MFMWTFSPGAFLEIETNNYKKLFLAIPLPVPPFAQAPMAQVQLVQSGGAVVQPRSLRLS 60
|||||
1 MMTITSPFGAFLEIETNNYKKLFLAIPLPVPPFAQAPMAQVQLVQSGGAVVQPRSLRLS 60

QY 61 CAASGFIFFSSYGNHWVQAQPGKGLBKVAGIIFYDGKNKYADSVKGRFTISRDSKNTLYL 120
61 CAASGFIFFSYGNHWVQAQPGKGLBKVAGIIFYDGKNKYADSVKGRFTISRDSKNTLYL 120

Dd 121 QMNSLAEDTAVYYCARDRGYYTMDYWKGGKTTVTVSSGGGSGGGGSGGSGSGLTQPP 180
121 QMNSLAEDTAVYYCARDRGYYTMDYWKGGKTTVTVSSGGGSGGGGSGGSGSGLTQPP 180

QY 181 SVSGARGGVVITSCGRSSNIGAGHDVHWYQOLDEGTAPKLLITPDSSNRPSGVDPFGSGR 240
181 SVSGARGGVVITSCGRSSNIGAGHDVHWYQOLDEGTAPKLLITPDSSNRPSGVDPFGSGR 240

Dd 241 SGTSSALATITGLQAEDEADYVQSYDSSLRGSYFGGKTYTVLGAANHHNHGAAEQKL 300
241 SGTSSALATITGLQAEDEADYVQSYDSSLRGSYFGGKTYTVLGAANHHNHGAAEQKL 300

QY 301 ISEEDLNGAA 310
301 ISEEDLNGAA 310

Dd 301 ISEEDLNGAA 310

RESULT 3
US-10-288-917-9
; Sequence 9, Application US/10288917
; Publication No. US20030148455A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; Chuntarapal, Anan
; Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/288,917
; FILING DATE: 06-NO. US20030148455A1-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/052798
; FILING DATE: 02-NOV-2001

```

APPLICATION NUMBER: 09/079029
FILING DATE: 14-MAY-1998
APPLICATION NUMBER: 60/074119
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 60/046615
FILING DATE: 15-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-288-917-9

Query Match 75.2%; Score 1231.5; DB 12; Length 309;
Best Local Similarity 78.0%; Pred. No. 1e-77;
Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

QY 1 MTMTTPSGAFLEIFENFKLLFAIPLVPPYPAAPAMAQVOLVOSGGGVOPGSLRLS 60
DB 1 MTMTTPSGAFLEIFENFKLLFAIPLVPPYPAAPAMAQVOLVOSGGGVOPGSLRLS 60
QY 61 CAASGFIFSSYGMHVRQAPGKLEWAGIFYDGKNTYADSVKGRFTISRDNSKNTLYL 120
DB 61 CAASGFIFSSYGMHVRQAPGKLEWAGIFYDGKNTYADSVKGRFTISRDNSKNTLYL 120
QY 61 CAASGFIFSSYGMHVRQAPGKLEWAGIFYDGKNTYADSVKGRFTISRDNSKNTLYL 120
DB 61 CAASGFIFSSYGMHVRQAPGKLEWAGIFYDGKNTYADSVKGRFTISRDNSKNTLYL 120
QY 121 OMNSLRADTAVYYCAR---DRGYIYNDVWGKGTITVYSSGGGGSGGGSGGGSGQSVL 176
DB 121 OMNSLRADTAVYYCAR---DRGYIYNDVWGKGTITVYSSGGGGSGGGSGGGSGQSVL 176
QY 121 OMNSLRADTAVYYCAR---DRGYIYNDVWGKGTITVYSSGGGGSGGGSGGGSGQSVL 176
DB 121 OMNSLRADTAVYYCAR---DRGYIYNDVWGKGTITVYSSGGGGSGGGSGGGSGQSVL 176
QY 177 TOPPSVSGAPGQRTVYISCTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDDSNRPSGVPDRF 236
DB 177 TOPPSVSGAPGQRTVYISCTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDDSNRPSGVPDRF 236
QY 179 TOPPSVSGAPGQRTVYISCTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDDSNRPSGVPDRF 236
DB 179 TOPPSVSGAPGQRTVYISCTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDDSNRPSGVPDRF 236
QY 237 SGRSGTSASLAITGLQAEDEADYYCOSYDSSLRGSVFGGKTVTVLGAHHHHHNGAA 296
DB 237 SGRSGTSASLAITGLQAEDEADYYCOSYDSSLRGSVFGGKTVTVLGAHHHHHNGAA 296
QY 236 SGSSSGNTASLITITGAQAEDEADYYCNSRDSGNNHVVFGGKTLTVLGAHHHHHNGAA 295
DB 236 SGSSSGNTASLITITGAQAEDEADYYCNSRDSGNNHVVFGGKTLTVLGAHHHHHNGAA 295
QY 297 EQKLISEEDLNGAA 310
DB 297 EQKLISEEDLNGAA 310
QY 296 EQKLISEEDLNGAA 309
DB 296 EQKLISEEDLNGAA 309

RESULT 4

US-10-052-798-9
Sequence 9, Application US/10052798
Publication No. US20020150985A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilia W.
Ashkenazi, Avi J.
Chuncharapal, Anan
Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/052,798
FILING DATE: 02-NO. US20020150985A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-052-798-9

Query Match 75.2%; Score 1231.5; DB 14; Length 309;
Best Local Similarity 78.0%; Pred. No. 1e-77;
Matches 245; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

QY 1 MTMTTPSGAFLEIFENFKLLFAIPLVPPYPAAPAMAQVOLVOSGGGVOPGSLRLS 60
DB 1 MTMTTPSGAFLEIFENFKLLFAIPLVPPYPAAPAMAQVOLVOSGGGVOPGSLRLS 60
QY 61 CAASGFIFSSYGMHVRQAPGKLEWAGIFYDGKNTYADSVKGRFTISRDNSKNTLYL 120
DB 61 CAASGFIFSSYGMHVRQAPGKLEWAGIFYDGKNTYADSVKGRFTISRDNSKNTLYL 120
QY 61 CAASGFIFSSYGMHVRQAPGKLEWAGIFYDGKNTYADSVKGRFTISRDNSKNTLYL 120
DB 61 CAASGFIFSSYGMHVRQAPGKLEWAGIFYDGKNTYADSVKGRFTISRDNSKNTLYL 120
QY 121 OMNSLRADTAVYYCAR---DRGYIYNDVWGKGTITVYSSGGGGSGGGSGGGSGQSVL 176
DB 121 OMNSLRADTAVYYCAR---DRGYIYNDVWGKGTITVYSSGGGGSGGGSGGGSGQSVL 176
QY 121 OMNSLRADTAVYYCAR---DRGYIYNDVWGKGTITVYSSGGGGSGGGSGGGSGQSVL 176
DB 121 OMNSLRADTAVYYCAR---DRGYIYNDVWGKGTITVYSSGGGGSGGGSGGGSGQSVL 176
QY 177 TOPPSVSGAPGQRTVYISCTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDDSNRPSGVPDRF 236
DB 177 TOPPSVSGAPGQRTVYISCTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDDSNRPSGVPDRF 236
QY 179 TOPPSVSGAPGQRTVYISCTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDDSNRPSGVPDRF 236
DB 179 TOPPSVSGAPGQRTVYISCTGRSSNIGAGHDVHWYQQLPCTAPKLLIYDDSNRPSGVPDRF 236
QY 237 SGRSGTSASLAITGLQAEDEADYYCOSYDSSLRGSVFGGKTVTVLGAHHHHHNGAA 296
DB 237 SGRSGTSASLAITGLQAEDEADYYCOSYDSSLRGSVFGGKTVTVLGAHHHHHNGAA 296
QY 236 SGSSSGNTASLITITGAQAEDEADYYCNSRDSGNNHVVFGGKTLTVLGAHHHHHNGAA 295
DB 236 SGSSSGNTASLITITGAQAEDEADYYCNSRDSGNNHVVFGGKTLTVLGAHHHHHNGAA 295
QY 297 EQKLISEEDLNGAA 310
DB 297 EQKLISEEDLNGAA 310
QY 296 EQKLISEEDLNGAA 309
DB 296 EQKLISEEDLNGAA 309

RESULT 5

US-10-288-917-10
Sequence 10, Application US/10288917
Publication No. US2003014845A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilia W.
Ashkenazi, Avi J.
Chuncharapal, Anan
Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/288,917
FILING DATE: 06-NOV-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/052798
FILING DATE: 02-NOV-2001
APPLICATION NUMBER: 09/079029
FILING DATE: 14-MAY-1998
APPLICATION NUMBER: 60/074119
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 60/046615
FILING DATE: 15-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-288-917-10

Query Match 75.2%; Score 1231; DB 12; Length 312;

Best Local Similarity 77.7%; Pred. No. 1,1e-77;
Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;

QY 1 MTMTIPSGAFLEIFNNKKLFAIPVPPFYAAPAMAQVQLVSGGCVVPGGRSLRLS 60
DB 1 MTMTIPSGAFLEIFNNKKLFAIPVPPFYAAPAMAQVQLVSGGCVVPGGRSLRLS 60
QY 61 CAASGFTSSYGMHVRQAPGKGLVAGIFDGNKYYADSVKGRFTISRDNKNTLYL 120
DB 61 CAASGFTSSYGMHVRQAPGKGLVAGIFDGNKYYADSVKGRFTISRDNKNTLYL 120
QY 121 QNLSLRADTAVYYCARD-----RGYYMDVNGKFTVTVSSGGSGSGSGSGGS 172
DB 121 QNLSLRADTAVYYCARD-----RGYYMDVNGKFTVTVSSGGSGSGSGSGGS 172
QY 173 QSVLTQPPSVSGAPQORYTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDSSNRPSGV 232
DB 173 QSVLTQPPSVSGAPQORYTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDSSNRPSGV 232
QY 233 PDRFSGSSGTSASLITGLQAEADYDYCQSYDSSLRGVSFGGKTATVLCGAAHHHHH 292
DB 233 PDRFSGSSGTSASLITGLQAEADYDYCQSYDSSLRGVSFGGKTATVLCGAAHHHHH 292
QY 293 HGAEOKLISEEDLNGAA 310
DB 293 HGAEOKLISEEDLNGAA 312

RESULT 6

US-10-052-798-10

Sequence 10, Application US/10052798

Publication No. US20020150985A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

Chuntharapat, Anan

Kim, Kyung J.

TITLE OF INVENTION: Apo-2 Receptor

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/052,798
FILING DATE: 02-NOV-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-052-798-10

Query Match 75.2%; Score 1231; DB 14; Length 312;

Best Local Similarity 77.7%; Pred. No. 1,1e-77;
Matches 247; Conservative 15; Mismatches 42; Indels 14; Gaps 4;

QY 1 MTMTIPSGAFLEIFNNKKLFAIPVPPFYAAPAMAQVQLVSGGCVVPGGRSLRLS 60
DB 1 MTMTIPSGAFLEIFNNKKLFAIPVPPFYAAPAMAQVQLVSGGCVVPGGRSLRLS 60
QY 61 CAASGFTSSYGMHVRQAPGKGLVAGIFDGNKYYADSVKGRFTISRDNKNTLYL 120
DB 61 CAASGFTSSYGMHVRQAPGKGLVAGIFDGNKYYADSVKGRFTISRDNKNTLYL 120
QY 121 QNLSLRADTAVYYCARD-----RGYYMDVNGKFTVTVSSGGSGSGSGSGGS 172
DB 121 QNLSLRADTAVYYCARD-----RGYYMDVNGKFTVTVSSGGSGSGSGSGGS 172
QY 173 QSVLTQPPSVSGAPQORYTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDSSNRPSGV 232
DB 173 QSVLTQPPSVSGAPQORYTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDSSNRPSGV 232
QY 233 PDRFSGSSGTSASLITGLQAEADYDYCQSYDSSLRGVSFGGKTATVLCGAAHHHHH 292
DB 233 PDRFSGSSGTSASLITGLQAEADYDYCQSYDSSLRGVSFGGKTATVLCGAAHHHHH 292
QY 293 HGAEOKLISEEDLNGAA 310
DB 293 HGAEOKLISEEDLNGAA 312

RESULT 7

US-09-880-748-1519

Sequence 1519, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS

FILE REFERENCE: P5523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

RESULTS


```
Db      121 GGGGGGGGGGGGSSQSVLTQPPSVSGAPGGRVTISCTGRSSNIGAGFDVHWYQLPGRRA 180
QY      218 PKLIYDSDNRPSGVDPFRSGSRSGTASLAITGLQADEADYYCOASVDSLRSGVEGCG 277
Db      181 PKVLYGNSNRPSSGVDPFRSGSKSGTSASLAITGLQADEADYYCOASVDSLRRAVFGSTG 240
QY      278 TKVTVLGG 284
Db      241 TKVTVLGG 247

RESULT 13
US-09-880-748-1841
; Sequence 1841, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that immunospecifically bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1841
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1841

Query Match      64.3%; Score 1053.5; DB 11; Length 258;
Best Local Similarity 80.2%; Pred. No. 1.6e-65;
Matches 207; Conservative 17; Mismatches 21; Indels 13; Gaps 4;

QY      40 OVOLVOSGGGVOPGRSRLSCAASGFIFSSYGMHWVQAPGKGLEWAGIFDYDGNK-- 97
Db      1 EVOLVETGGGLVKPEGSLRLSCAASGFIFSSYGMHWVLPAPGKGLEWASIRSRSGTYI 60
QY      98 YYADSVKGRFTTISRDNKNTLYLQNSLRAEDTAVYYCARD-----RGYYY--MDVM 147
Db      61 YYADSVKGRFTTISRDNKNTLYLQNSLRAEDTAVYYCARDPQNDILTGYYYYGMDVM 120
QY      148 GKGTTVVYSSGGGGGGGGGGGGGGS-QSVLTQPPSVSGAPGGRVTISCTGRSSNIGACHD 206
Db      121 GCGTLVTVSSGGGGGGGGGGGGAQVLTQPPSSVSGAPGGRVTIPCTGSSSNIRAGYD 180
QY      207 VHWYQQLPGTAPKLIYDSDNRPSGVDPFRSGSRSGTASLAITGLQADEADYYCOASYD 266
Db      181 VHWYQQLPGTAPKLIYDSDNRPSGVDPFRSGSKSGTSASLAITGLQADEADYYCOASYD 240
QY      267 SLSRGSVFGGGTKVTVLGG 284
Db      241 TNLGSMWVFGGGTKLTVLGG 258

RESULT 14
US-09-880-748-1458
; Sequence 1458, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that immunospecifically bind Blys
; FILE REFERENCE: PF523
```

```
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1458
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1458

Query Match      64.1%; Score 1050.5; DB 11; Length 260;
Best Local Similarity 78.5%; Pred. No. 2.6e-65;
Matches 205; Conservative 17; Mismatches 22; Indels 17; Gaps 4;

QY      40 OVOLVOSGGGVOPGRSRLSCAASGFIFSSYGMHWVQAPGKGLEWAGIFYD-CGNKY 98
Db      1 OVOLVOSGGGVOPGRSRLSCAASGFIFRYSAMSWVQAPGKGLEWVSGISGNAGSNKY 60
QY      99 YADSVKGRFTTISRDNKNTLYLQNSLRAEDTAVYYCARD-----GYYY-- 143
Db      61 YADSVKGRFTTISRDNKNTLYLQNSLRAEDTAVYYCARDPGSEYDILTGYLEFYYYG 120
QY      144 MDVWGKGTTVVSSGGGGGGGGGGGGSQSVLTQPPSVSGAPGGRVTISCTGRSSNIGA 203
Db      121 MDVWGQGTMTVTVSSGGGGGGGGGGGGSQSVLTQPPASGPGGRVTISCSGSSNIGS 180
QY      204 GHVHWYQQLPGTAPKLIYDSDNRPSGVDPFRSGSRSGTASLAITGLQADEADYYCQ 263
Db      181 NTVMWYQRLRGAAPQLLITNNQRPSSGTPFRFSKSGTSGSLVTSGLQDEADYYCA 239
QY      264 SYDSSLRGSVFGGGTKVTVLGG 284
Db      240 SWDSSLNGRVFGGGTKLTVLGG 260

RESULT 15
US-09-880-748-839
; Sequence 839, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that immunospecifically bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 839
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-839
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OW protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 20.9774 Seconds
(without alignments)
1421.159 Million cell updates/sec

Title: US-10-052-798-11

Perfect score: 1638

Sequence: 1 MTMTTSPGAFLEIFNVKK.....HHGAPDKLISEEDLNGAA 310

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	750.5	45.8	268	2	A56446
2	619	37.8	249	2	S41374
3	569	34.7	128	2	S48797
4	560	34.2	122	2	E36005
5	556	33.9	233	2	JC5322
6	555.5	33.9	123	2	S38493
7	545.5	33.3	132	2	S31603
8	544	33.2	118	2	S31116
9	541.5	33.1	121	2	S19666
10	541	33.0	121	2	S51148
11	541	33.0	140	2	S70442
12	540.5	33.0	121	2	G36005
13	539	32.9	122	2	S31117
14	537	32.8	130	2	S31601
15	533.5	32.6	119	2	F36005
16	533.5	32.6	133	2	A49028
17	531.5	32.4	111	2	S36274
18	530	32.4	114	2	S46390
19	528	32.2	114	2	S46392
20	526.5	32.1	134	2	S31679
21	520	31.7	147	2	I37780
22	519.5	31.7	113	2	S38490
23	519	31.7	139	2	S31674
24	518.5	31.7	111	2	PH1645
25	517	31.6	236	2	S25746
26	516	31.5	137	2	S31701
27	514.5	31.4	130	2	PL0098
28	511.5	31.2	135	2	S31598
29	511	31.2	114	2	S46391

30	511	31.2	120	2	S31112	Ig heavy chain - h
31	508	31.0	108	2	PH1642	Ig heavy chain V r
32	507.5	31.0	125	2	S37455	Ig mu chain - huma
33	506.5	30.9	117	2	S36259	Ig heavy chain V r
34	504.5	30.8	138	2	S31666	Ig heavy chain V r
35	504	30.8	120	2	S48798	Ig heavy chain V r
36	503.5	30.7	160	2	S05271	Ig heavy chain pre
37	503	30.7	122	1	M3H0M	Ig heavy chain V-I
38	502	30.6	119	2	S31111	Ig heavy chain - h
39	501.5	30.6	119	2	S31107	Ig heavy chain - h
40	500.5	30.6	111	2	PH1643	Ig heavy chain V r
41	499.5	30.5	115	2	S36284	Ig heavy chain V r
42	499.5	30.5	122	2	S31119	Ig heavy chain - h
43	499	30.5	133	2	S31510	Ig heavy chain - h
44	496.5	30.3	120	2	S36278	Ig heavy chain V r
45	496	30.3	151	2	A60943	Ig heavy chain pre

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)

C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C:Accession: A56446

R:Yang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity dioxin-binding protein displayed on M13 is functionally ide

A:Reference number: A56446; MUID:95229583; PMID:7713873

A:Accession: A56446

A:Molecule type: mRNA

A:Residues: 1-268 <TAN>

A:Cross-references: GB:U20617

C:Keywords: heterotetramer; immunoglobulin

Query Match 45.8%; Score 750.5; DB 2; Length 268;

Best Local Similarity 55.2%; Pred. No. 2.1e-43;

Matches 153; Conservative 36; Mismatches 75; Indels 13; Gaps 5;

QY	38	MAOVOLVSGGCVOPGRSLRLSCAASGFIPTSGYGMHWVRQAPGKLEWVAGIFYDGSK	97
DB	1	MAQYKLDGSAELVYKPGASVYKLTCTSGFNKIDYIMHWVKRPGGLEIMIGRIAPANGIT	60
QY	98	YYADSVKGRFTISRDNSKNTLYIQMNSIRAEDEVYICARDGY--YMDVWKGKPTVT	154
DB	61	KYDKPFGKATIAADTSNTAVYLQSLTSDTAVYCA--SYLLREYENYMGOGTTVT	117
QY	155	VSSGGGGGGGGGGGGGQSIVLTQPPSV-SCAPQQRVYISTGGRSSNIGAGHDVHWVQOL	213
DB	118	VSSGGGGGGGGGGGGGDIETQSPALMSASIDEKVMVSCRASS---VNFYVYQOK	173
QY	214	PGTAPKLLTYDSDNRPSPGSRGSGTASLAITGLADEADADYCCOSYDSLSRGSV	273
DB	174	SDASPKLVYTTSHLPVPRPARFSGSGSGNSYSLTISMBEDADATYYCOQFTSS--PFT	231
QY	274	FGGGTKVTVLCAAAHHHHHNGAEDQKLISEEDLNGAA	310
DB	232	FGSGTKLEIKRSAAHHHHHNGAEDQKLISEEDLNGAA	268

RESULT 2
S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Arsenanko, O.; Weller, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv anti

A;Accession: S41374
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <ART>
A;Cross-references: EMBL:Z29480

Query Match	37.88;	Score 619;	DB 2;	Length 249;
Best Local Similarity	53.48;	Pred. No. 1.3e-34;		
Matches 134;	Conservative 31;	Mismatches 80;	Indels 6;	Gaps 4

[illegible]

RESULT 3
S48797
Ig heavy chain V region (anti-Sm, VH3/DxP4/JH6) - human (fragment)
G: Good, N: None, S: Surface, T: Transmembrane, I: Intracellular

C:Date: 13-Jan-1995 #sequenceRevision 13-Sep-1998 #textChange 23-Jul-1999
C:Accession: S48797; S26893
R:Mamoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S48797
A:Molecule type: mRNA
A:Residues: 1-128 <MAH>
A:Cross-references: EMBL:Z46379; NID:G587147; PIDN:CAA86512.1; PID:G1340168
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline VH sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26893
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12350; NID:G32922; PIDN:CAA78220.1; PID:G32923
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
C:15-98/Domain: immunoglobulin homology <IMM>

[illegible]

RESULT 4
E36005
Ig heavy chain V region (W72) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1990

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable 9
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: E36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <SCH>
A:Cross-references: GB:M34030
C:Genetics:
A:Gene: GDB:IGHF, IGHDI
A:Cross-references: GDB:118731, OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IM>

Query Match	34.28;	Score 560;	DB 2;	Length 122;
Best Local Similarity	89.38;	Pred. No. 5.5e-31;		
Matches 109; Conservative	2;	Mismatches 7;	Indels 4;	Gaps 1

[illegible]

RESULT 5
JC5322
p53 specific single-chain antibody pab421 - human
C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R:Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scrv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MUID:97168950; PMID:9016757
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
A:Experimental source: hybridoma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It res

C:Accession: S51148
R:de Kruijf, J.; Boel, E.; Logtenberg, T.
submitted to the EMBL Data Library, January 1995
A:Description: Selection and application of human SCRV antibody fragments from a semi-sy
A:Reference number: S51147
A:Accession: S51148
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <DEK>
A:Cross-references: EMBL:X83713
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
F:13-90/Domain: Immunoglobulin homology <IMM>

Query Match 33.0%; Score 541; DB 2; Length 112;
Best Local Similarity 92.8%; Pred. No. 9.4e-30;
Matches 103; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 176 LTOPPSVSGAPGQRTVISTGSSNIGAGHDVHWYQQLPGTAKLLIYDSSNPPSPVR 235
|||||
DB 2 LTOPPSVSGAPGQRTVISTGSSNIGAGDVHWYQQLPGTAKLLIYDSSNPPSPVR 61
|||||

QY 236 FSGSRGTSASLAITGLQADEADYCCQSYDSSLRGSFVGCGTKVTVLGAA 286
|||||
DB 62 FSGSRGTSASLAITGLQADEADYCCQSYDSSLRGSFVGCGTKVTVLGAA 112
|||||

RESULT 11
S70442
Ig heavy chain precursor V region (nu) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C:Accession: S70442
R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A:Title: IGM kappa/Jambda EBV human B cell clone: an early step of differentiation of fe
A:Reference number: S70442; MID:93024508; PMID:1383655
A:Accession: S70442
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
F:34-117/Domain: Immunoglobulin homology <IMM>

Query Match 33.0%; Score 541; DB 2; Length 140;
Best Local Similarity 86.8%; Pred. No. 1.2e-29;
Matches 105; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

QY 40 QVOLVSGGGVQPGRSRLRSCASGFIFSSYGMHWVROAPGKLEWVAGIFYDGNKXY 99
|||||
DB 20 QVOLVSGGGVQPGRSRLRSCASGFIFSSYGMHWVROAPGKLEWVAFIRYDGNKXY 79
|||||

QY 100 ADSVKGRFTISRNSKNTLYLQKNSLRADETAVYYCARDR--GYIYMDVWGKGTIVYVS 157
|||||
DB 80 ADSVKGRFTISRNSKNTLYLQKNSLRADETAVYYCARDHIVGATFYDWGQGTIVYVS 139
|||||

QY 158 G 158
DB 140 G 140

RESULT 12
G36005
Ig heavy chain V region (M74) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: G36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MID:90349571; PMID:2117273
A:Accession: G36005
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-121 <SCH>
A:Cross-references: GB:M34031
C:Genetics:
A:Gene: GDB:IGH4; IGHDX1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 33.0%; Score 540.5; DB 2; Length 121;
Best Local Similarity 86.8%; Pred. No. 1.1e-29;
Matches 105; Conservative 3; Mismatches 10; Indels 3; Gaps 1;

QY 40 QVOLVSGGGVQPGRSRLRSCASGFIFSSYGMHWVROAPGKLEWVAGIFYDGNKXY 99
|||||
DB 1 QVOLVSGGGVQPGRSRLRSCASGFIFSSYGMHWVROAPGKLEWVAVISYDGNKXY 60
|||||

QY 100 ADSVKGRFTISRNSKNTLYLQKNSLRADETAVYYCARDR--GYIYMDVWGKGTIVYVS 156
|||||
DB 61 ADSVKGRFTISRNSKNTLYLQKNSLRADETAVYYCARDKRWGALFDYWGQGTIVYVS 120
|||||

QY 157 S 157
DB 121 S 121

RESULT 13
S31117
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31117
R:Raphoport, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A:Reference number: S31104; MID:92111633; PMID:1730252
A:Accession: S31117
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-122 <RAA>
A:Cross-references: EMBL:X62967
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 32.9%; Score 539; DB 2; Length 122;
Best Local Similarity 85.2%; Pred. No. 1.4e-29;
Matches 104; Conservative 5; Mismatches 9; Indels 4; Gaps 1;

QY 40 QVOLVSGGGVQPGRSRLRSCASGFIFSSYGMHWVROAPGKLEWVAGIFYDGNKXY 99
|||||
DB 1 QVOLVSGGGVQPGRSRLRSCASGFIFSSYGMHWVROAPGKLEWVAVIWDGSKXY 60
|||||

QY 100 ADSVKGRFTISRNSKNTLYLQKNSLRADETAVYYCARD--GYIYMDVWGKGTIVYVS 155
|||||
DB 61 ADSVKGRFTISRNSKNTLYLQKNSLRADETAVYYCARDFFAPPNMSEHDYWGQGTIVYVS 120
|||||

QY 156 SS 157
DB 121 SS 122

RESULT 14
S31601
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31601
R:Cuisinier, A.M.; Gauthier, L.; Boudli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from t

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:03 ; Search time 11.6541 seconds

(without alignments)
1250.910 Million cell updates/sec

Title: US-10-052-798-11

Perfect score: 1638
Sequence: 1 MTMTSPSCAFLEIFNVKK.....HHGAAEQKLSEEDLNGAA 310

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0.5
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	503	30.7	122 1	HV3G_HUMAN
2	484.5	29.6	121 1	HV3J_HUMAN
3	482	29.4	126 1	HV3K_HUMAN
4	470.5	28.7	119 1	HV3I_HUMAN
5	460	28.1	122 1	HV3H_HUMAN
6	449.5	27.4	130 1	LV1G_HUMAN
7	447	27.3	136 1	HV16_MOUSE
8	445	27.2	112 1	LV1H_HUMAN
9	442.5	27.0	111 1	LV1D_HUMAN
10	439	26.8	116 1	HV3E_HUMAN
11	431.5	26.3	115 1	HV3F_HUMAN
12	429	26.2	117 1	HV3C_HUMAN
13	427.5	26.1	111 1	LV1C_HUMAN
14	426.5	26.0	109 1	LV1F_HUMAN
15	426.5	26.0	120 1	HV3E_HUMAN
16	424	25.9	112 1	LV1B_HUMAN
17	423.5	25.9	103 1	LV1E_HUMAN
18	423	25.8	114 1	HV3B_HUMAN
19	422	25.8	120 1	HV3U_HUMAN
20	420	25.6	119 1	HV3M_HUMAN
21	419.5	25.6	119 1	HV3L_HUMAN
22	418	25.5	119 1	HV3N_HUMAN
23	415.5	25.4	111 1	LV1A_HUMAN
24	414.5	25.3	116 1	HV05_CARAU.
25	413.5	25.2	109 1	LV1I_HUMAN
26	413.5	25.2	115 1	HV3D_HUMAN
27	413	25.2	117 1	HV38_MOUSE
28	411	25.1	117 1	HV3O_HUMAN
29	408	24.9	122 1	HV20_MOUSE
30	406.5	24.8	123 1	HV18_MOUSE
31	406.5	24.8	123 1	HV19_MOUSE
32	405	24.7	122 1	HV21_MOUSE
33	403.5	24.6	123 1	HV24_MOUSE

34	402	24.5	122 1	HV3A_HUMAN	P01762	homo sapien
35	401.5	24.5	123 1	HV23_MOUSE	P01792	mus musculus
36	401.5	24.5	123 1	HV25_MOUSE	P01794	mus musculus
37	400.5	24.5	123 1	HV22_MOUSE	P01791	mus musculus
38	396	24.2	119 1	HV40_MOUSE	P01810	mus musculus
39	393	24.0	112 1	LV2K_HUMAN	P04209	homo sapien
40	392	23.9	119 1	HV37_MOUSE	P01807	mus musculus
41	390.5	23.8	111 1	LV2D_HUMAN	P01707	homo sapien
42	390.5	23.8	117 1	HV02_CANFA	P01785	canis famill
43	390.5	23.8	142 1	HV01_RAT	P01805	rattus norv
44	390	23.8	117 1	HV55_MOUSE	P18526	mus musculus
45	388	23.7	117 1	HV54_MOUSE	P18525	mus musculus

ALIGNMENTS

RESULT 1	HV3G_HUMAN	STANDARD;	PRT;	122 AA.
AC	P01768:			
DP	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig heavy chain V-II region CAM.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=81013859; PubMed=6774332;			
RA	Lehman D.W., Putnam F.W.;			
RT	"Antino acid sequence of the variable region of a human mu chain:			
RT	location of a possible JH segment."			
RL	Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).			
CC	!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A			
CC	PATIENT WITH MACROGLOBULINEMIA.			
CC	!- SIMILARITY: Contains 1 immunoglobulin-like domain.			
DR	PIR: A02051, M3HUM.			
DR	HSSP; P01772; ZFB4.			
DR	GO: GO:0005576; C:extracellular; NAS.			
DR	GO: GO:0003823; F:antigen binding activity; NAS.			
DR	GO: GO:0006955; P:Immune response; NAS.			
DR	InterPro: IPR007110; Ig-like.			
DR	InterPro: IPR003006; Ig-MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	PIfam; PF00047; Ig; 1.			
DR	SMART; SM00406; Igv; 1.			
KW	PROSITE: PS50835; IG LIKE; 1.			
RV	Immunoglobulin V region; Pyroliidone carboxylic acid.			
FT	DOMAIN 1 112			
FT	WQW_RES 1 1			
FT	NON_TER 122			
FT	SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;			

Query March 30.7%; Score 503; DB 1; Length 122;
Best Local Similarity 77.0%; Pred. No. 4.4e-30;
Matches 94; Conservative 12; Mismatches 12; Indels 4; Gaps 1;

QY	40 QVQLVSGGQVYVQGRSLRLSCAASGFFSSYGHWYRQAPGKLELVAVGIFDYDGKNTY 99
DB	1 QVELVESGGGVYVZGGRSLRLSCAASGFFFSYVAHWYRQPGKLELVAVISYGBBKY 60
QY	100 ADSYKGRFTISRDNSKNTLYIQANSLRAEDTAVYTCARDR---GYTMDYWGKITYY 155
DB	61 ABSYKGRFTISRDNSKNTLYIQANSLRAEDTAVYTCARDR---GYTMDYWGKITYY 120
QY	156 SS 157
DB	121 SS 122

```

RESULT 2
HV31_HUMAN
ID HV31_HUMAN STANDARD: PRT; 121 AA.
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region HLL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
RT cryoimmunoglobulin IgG H1."
RL Biochemistry 18:553-560(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02054; GIHURL.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyroliidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT NON_TER 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610E5DAB CRC64;

Query Match
Best Local Similarity 29.6%; Score 484.5; DB 1; Length 121;
Matches 92; Conservative 9; Mismatches 17; Indels 3; Gaps 1;

QY 40 OVQLVOSGGVQVQPGSRSLRLSCAASGFFESYGHWVRQAPGKLEWVAGIFYDGKNTY 99
DB 1 OVQLVQAGGGVQVQPGSRSLRLSCAASGFFESYNGHWVRQAPGKLEWVAVIYNGSRITY 60
QY 100 ADVKAGRTTISRDNKNTLYLQMSLRAEDTAVYYCARDRGY---YYMDVWGKGTYYVS 156
DB 61 GDSVAGRTTISRDNKNTLYLQMSLRAEDTAVYYCARDPDLITAFSPDYGQGLVTVS 120
QY 157 S 157
DB 121 S 121
Db 121 S 121

RESULT 3
HV3K_HUMAN
ID HV3K_HUMAN STANDARD: PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=688494;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary

```

```

RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marguerat M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution."
RL J. Mol. Biol. 141:369-391(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02055; GIHURL.
DR PDB; 2FB4; 12-JUL-89.
DR PDB; 2IG2; 12-JUL-89.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG-LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyroliidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT STRAND 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT HELIX 62 64
FT STRAND 65 65
FT TURN 66 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT STRAND 88 90
FT HELIX 92 99
FT STRAND 106 106
FT STRAND 107 108
FT TURN 109 109
FT STRAND 113 116
FT STRAND 120 124
FT NON_TER 126
SQ SEQUENCE 126 AA; 13718 MW; EAD71B52B16F8776 CRC64;

Query Match
Best Local Similarity 29.4%; Score 482; DB 1; Length 126;
Matches 93; Conservative 14; Mismatches 11; Indels 8; Gaps 1;

QY 40 OVQLVOSGGVQVQPGSRSLRLSCAASGFFESYGHWVRQAPGKLEWVAGIFYDGKNTY 99
DB 1 OVQLVESGGVQVQPGSRSLRLSCSSGFFESYAMTWVRQAPGKLEWVAIIMDGSDOHY 60
QY 100 ADVKAGRTTISRDNKNTLYLQMSLRAEDTAVYYCARDRGY-----DYWGKGT 151
DB 61 ADVKAGRTTISRDNKNTLYLQMSLRAEDTAVYYCARDGSGHGCSSASCGPDPYWGQGT 120
QY 152 TVTVSS 157
DB 121 PTVVSS 126
Db 121 PTVVSS 126

RESULT 4
HV31_HUMAN

```

ID	SV1_HUMAN	STANDARD:	PRT:	119 AA.
AC	P01770:			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	Ig heavy chain V-III region NIE.			
OS	Homo sapiens (Human).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid:9606;			
RN	(1)			
RP	SEQUENCE.			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The role of antibody structure. The primary structure of a			
RT	monoclonal IgG1 immunoglobulin (myeloma protein N1e). III. The			
RT	chymotryptic peptides of the H-chain, alignment of the tryptic			
RL	peptides and discussion of the complete structure";			
RL	Hoppe-seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[2]			
RP	DISULFIDE BOND.			
RX	MEDLINE=77070267; PubMed=1002129;			
RA	Dreher L., Schwarz J., Reichel W., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal			
RT	IgG1 immunoglobulin (myeloma protein N1e), I. Purification and			
RT	characterization of the protein, the L- and H-chains, the			
RT	cyanogen bromide cleavage products, and the disulfide bridges.";			
RL	Hoppe-seyler's Z. Physiol. Chem. 357:1515-1540(1976).			
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA			
CC	PROTEIN.			
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.			
PC	PIR: A91668; GIHUNI.			
DR	HSSP; P01772; 2FB4.			
DR	GO: GO:0005576; C:extracellular; NAS.			
DR	GO: GO:0003823; F:antigen binding activity; NAS.			
DR	GO: GO:0006955; P:immune response; NAS.			
DR	InterPro: IPR007110; Ig-like.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
KW	PROSITE: PS50835; IG-LIKE; 1.			
DR	Immunoglobulin V region; Pyroglutamate carboxylic acid.			
FT	DOMAIN	1	112	
FT	MOD_RES	1	1	
FT	DISULFID	22	96	
FT	NON_TER	119	119	
SO	SEQUENCE	119 AA;	13242 MW;	C96935A6E55E165B CRC64;
	Query Match	28.7%;	Score 470.5;	DB 1; Length 119;
	Best Local Similarity	76.7%;	Pred. No. 9, 8e-28;	
	Matches	92; Conservative	10; Mismatches	15; Indels 3; Gaps 2
QY	40	QVOLTQSGGVQPERSLRLCAASGCTFFSSVGMHVRAPRQKGLQEWAGIFPDGKNKY	99	
DB	1	QVOLTQSGGVQPERSLRLCAASGCTFFSRTTTHMVRAPRQKGLQEWAVMSYBGBKH	60	
QY	100	ADSVAGRTTISRDNKNTLYLQMSLRARQEDTAVYYCA--RDGGYYMDVWGKGTFTVSS	157	
DB	61	ADSVAGRTTISRDNKNTLYLQMSLRARQEDTAVYYCARIRDTAMFFAH-WGGQTLTVSS	119	
	RESULT 5			
AC	SV3H_HUMAN	STANDARD:	PRT:	122 AA.
AC	P01769:			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	Ig heavy chain V-III region GA.			
OS	Homo sapiens (Human).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			

```

OX NCB1_TextID=96606;
RN [1]
RN SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL Biochemistry 13:2482-2498(1974).
CC CC
CC 1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
CC 1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02052; M3HUGA.
DR HSSP: P01772; 2PBA.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-Like.
DR InterPro: IPR003006; IG-MHC.
DR InterPro: IPR003596; IG-V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG-LIKE; 1.
DR Immunoglobulin V region: Pyridone carboxylic acid.
DR DOMAIN 1 112
FT MOD_RES 1 122 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 1 122 IG-LIKE.
SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;

Query Match 28.1%; Score 460; DB 1; Length 122;
Best Local Similarity 68.9%; Pred. No. 5.8e-27;
Matches 84; Conservative 18; Mismatches 16; Indels 4; Gaps 1

OY 40 QVQLVQSGGSGGVQPGRLSLRSCAASGFTFSYGMHWQAPGKGLENVAGIFYDGNKRY 99
DB 1 QVZLVZSSGGAIVZPGRLSLRSCAASGFSFSTYAMHWQAPGKGLZMLSVISYBGBZLY 60
OY 100 ADSVKGRTTISRDNKNTLYIQMNSLRADETAVYICARD----KRTYMDWVGKTTVY 155
DB 61 AASVKGRTTISRBSKRTMYLEMNSLRAENTAVYVYCARSGIALGSVAGTDWVGZGLTVTI 120
OY 156 SS 157
DB 121 SS 122

RESULT 6
LV1G_HUMAN STANDARD; PRT; 130 AA.
ID LV1G_HUMAN
AC P06316;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region BL2 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
OC NCB1_TaxID=96606;
CC [1]
CC (SEQUENCE FROM N.A.
CC MEDLINE=85062823; PubMed=6095199;
CC Tsujimoto Y., Croce C.M.;
CC "Molecular cloning of a human immunoglobulin lambda chain variable
CC sequence.";
CC Nucleic Acids Res. 12:8407-8414(1984).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X01147 CAA25598.1; -

```

```

DR PIR; A01966; LIHUBL.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig-like.
DR InterPro; IPR003596; Ig-LV.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 130 IG LAMBDA CHAIN V-I REGION BL2.
FT DOMAIN 20 115 V SEGMENT.
FT DOMAIN 116 130 J SEGMENT.
FT DISULFID 41 108 BY SIMILARITY.
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 13564 MW; FA44BBL7D3A55BDF CRC64;

Query Match 27.4%; Score 449.5; DB 1; Length 130;
Best Local Similarity 74.1%; Pred. No. 3.6e-26;
Matches 86; Conservative 15; Mismatches 14; Indels 1; Gaps 1;

QY 169 GGGGSSVLTQPPSVSGAPGQRTISTGSSNNGAGHDVHWQQLPGLTPKLLIYDSSNR 228
DB 16 GMAOSVLTQPPSVSAPGQKVTISGSSSSNIGNDY-VSWYQVPGTAPKLLIYDNNKR 74
QY 229 PGGVPDRFSGSRSGTSASLAITGLQAEADADYCYCOSYDSSLRGVSFGGKTATVLG 284
DB 75 PGGVPDRFSGSRSGTSATITGLTGLQEDADYCCGTMNNSLGSWVFGGKTATVLG 130

RESULT 7
HVL6_MOUSE STANDARD; PRT; 136 AA.
ID HVL6_MOUSE
AC P01783;
DT 21-JUL-1986 (rel. 01, Last Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DE 15-SEP-2003 (rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Karl T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RT Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetungbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RT Nature 265:299-304(1977).
RN [3]
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00522; AAD15290.1; -
DR PIR; E90809; GIMS21.
DR PDB; 1IGC; 03-JUN-95.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.

```

```

DR InterPro; IPR003596; Ig-LV.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal: 3D-structure.
FT NON_TER 1 1
FT SIGNAL <1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 J44 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78
FT CONFLICT 89 90 HYAD -> DYAD (IN REF. 2).
FT CONFLICT 115 115 DN -> ND (IN REF. 2).
FT CONFLICT 120 120 W -> H (IN REF. 2).
FT NON_TER 136 136 Y -> W (IN REF. 2).
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 27.3%; Score 447; DB 1; Length 136;
Best Local Similarity 73.1%; Pred. No. 5.7e-26;
Matches 87; Conservative 12; Mismatches 18; Indels 2; Gaps 1;

QY 41 VOLVGGGVPGRSLRSCAASGFIFSSYGMHWVROAPGKLEWVGIFDGGNKRYA 100
DB 18 VOLVESGGGLVOPGGSRKLSCAASGFTSSFGMHVROAPEKGLWVAIISGSSTLHA 77
QY 101 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYGCAR--DRGYHYMDYWGKGTIVVSS 157
DB 78 DTVKGRFTISRNPNTLTFLQWTSLRSEDTAVYGCARNGNRYVAMDYWGQGTSTVVS 136

RESULT 8
LV1H_HUMAN STANDARD; PRT; 112 AA.
ID LV1H_HUMAN
AC P06887;
DT 01-JAN-1988 (rel. 06, Last Created)
DT 01-JAN-1988 (rel. 06, Last sequence update)
DE 15-SEP-2003 (rel. 42, Last annotation update)
DE Ig lambda chain V-I region MEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=85257662; PubMed=2410269;
RA Mhaesco E., Roy J.P., Congy N., Peran-Rivat L., Mhaesco C.;
RT "The amino acid sequence of a lambda light chain presenting abnormal
RT physicochemical and antigenic features.";
RT Eur. J. Biochem. 150:349-357(1985).
CC -1- MISCELLANEOUS: RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES
CC WERE POSITIONED BY HOMOLOGY.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
CC MARKERS.
CC -----
DR -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A25479; LIHDM.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig-Like.
DR InterPro; IPR003596; Ig-LV.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Monoclonal antibody;
KW Pyrolydione carboxylic acid.
FT DOMAIN 1 106
FT MOD_RES 1 1 IG-LIKE.
FT DISULFID 22 90 PYROLYDIONE CARBOXYLIC ACID.
FT NON_TER 112 112 BY SIMILARITY.
SQ SEQUENCE 112 AA; 11789 MW; 748124F079CFEB4 CRC64;

```

Query Match	Similarity	27.2%	Score 445:	DB 1:	Length 112:
Best Local	Similarity	76.6%	Pred. No. 6.4e-26:		
Matches	85:	Conservative	10:	Mismatches	16:
				Indels	0:
				Gaps	0:
QY	173	OSVLTOPPSVSGAGGAGORVYTCISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDDSNRPSGV	232		
DB	1	OSVLTOPPSAGTGGGRTVTCISGSSSNVGSNZPRAYWYQOLPGTAPKLLIYNNRPSGV	60		
QY	233	PDRSGSGSGTSASLAIITGLQAEDEADYCCSYDSSLGSVFGGCTKYTVL	283		
DB	61	PDRSGSGSGTSASLAIISGLQSEDEADYCAAMDSDLDGYVFGCTKYTVL	111		
RESULT 9					
QY	173	OSVLTOPPSVSGAGGAGORVYTCISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDDSNRPSGV	232		
DB	1	OSVLTOPPSAGTGGGRTVTCISGSSSNVGSNZPRAYWYQOLPGTAPKLLIYNNRPSGV	60		
QY	233	PDRSGSGSGTSASLAIITGLQAEDEADYCCSYDSSLGSVFGGCTKYTVL	283		
DB	61	PDRSGSGSGTSASLAIISGLQSEDEADYCAAMDSDLDGYVFGCTKYTVL	111		
RESULT 10					
QY	173	OSVLTOPPSVSGAGGAGORVYTCISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDDSNRPSGV	232		
DB	1	OSVLTOPPSVSAAPQOEYVTCISGSSSNIGG-DNFYSWYQOLPGTAPKLLIYNNRPSGI	59		
QY	233	PDRSGSGSGTSASLAIITGLQAEDEADYCCSYDSSLGSVFGGCTKYTVL	284		
DB	60	PDRSGSGSGTSASLAIITGLQDEADYCCYTWSSLSVGFEGGCTRYTVL	111		
RESULT 11					
QY	173	OSVLTOPPSVSGAGGAGORVYTCISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDDSNRPSGV	232		
DB	1	OSVLTOPPSAGTGGGRTVTCISGSSSNVGSNZPRAYWYQOLPGTAPKLLIYNNRPSGV	60		
QY	233	PDRSGSGSGTSASLAIITGLQAEDEADYCCSYDSSLGSVFGGCTKYTVL	283		
DB	61	PDRSGSGSGTSASLAIISGLQSEDEADYCAAMDSDLDGYVFGCTKYTVL	111		
RESULT 12					
QY	173	OSVLTOPPSVSGAGGAGORVYTCISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDDSNRPSGV	232		
DB	1	OSVLTOPPSAGTGGGRTVTCISGSSSNVGSNZPRAYWYQOLPGTAPKLLIYNNRPSGV	60		
QY	233	PDRSGSGSGTSASLAIITGLQAEDEADYCCSYDSSLGSVFGGCTKYTVL	283		
DB	61	PDRSGSGSGTSASLAIISGLQSEDEADYCAAMDSDLDGYVFGCTKYTVL	111		
RESULT 13					
QY	173	OSVLTOPPSVSGAGGAGORVYTCISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDDSNRPSGV	232		
DB	1	OSVLTOPPSAGTGGGRTVTCISGSSSNVGSNZPRAYWYQOLPGTAPKLLIYNNRPSGV	60		
QY	233	PDRSGSGSGTSASLAIITGLQAEDEADYCCSYDSSLGSVFGGCTKYTVL	283		
DB	61	PDRSGSGSGTSASLAIISGLQSEDEADYCAAMDSDLDGYVFGCTKYTVL	111		
RESULT 14					
QY	173	OSVLTOPPSVSGAGGAGORVYTCISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDDSNRPSGV	232		
DB	1	OSVLTOPPSAGTGGGRTVTCISGSSSNVGSNZPRAYWYQOLPGTAPKLLIYNNRPSGV	60		
QY	233	PDRSGSGSGTSASLAIITGLQAEDEADYCCSYDSSLGSVFGGCTKYTVL	283		
DB	61	PDRSGSGSGTSASLAIISGLQSEDEADYCAAMDSDLDGYVFGCTKYTVL	111		
RESULT 15					
QY	173	OSVLTOPPSVSGAGGAGORVYTCISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDDSNRPSGV	232		
DB	1	OSVLTOPPSAGTGGGRTVTCISGSSSNVGSNZPRAYWYQOLPGTAPKLLIYNNRPSGV	60		
QY	233	PDRSGSGSGTSASLAIITGLQAEDEADYCCSYDSSLGSVFGGCTKYTVL	283		
DB	61	PDRSGSGSGTSASLAIISGLQSEDEADYCAAMDSDLDGYVFGCTKYTVL	111		
RESULT 16					
QY	173	OSVLTOPPSVSGAGGAGORVYTCISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDDSNRPSGV	232		
DB	1	OSVLTOPPSAGTGGGRTVTCISGSSSNVGSNZPRAYWYQOLPGTAPKLLIYNNRPSGV	60		
QY	233	PDRSGSGSGTSASLAIITGLQAEDEADYCCSYDSSLGSVFGGCTKYTVL	283		
DB	61	PDRSGSGSGTSASLAIISGLQSEDEADYCAAMDSDLDGYVFGCTKYTVL	111		
RESULT 17					
QY	173	OSVLTOPPSVSGAGGAGORVYTCISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDDSNRPSGV	232		
DB	1	OSVLTOPPSAGTGGGRTVTCISGSSSNVGSNZPRAYWYQOLPGTAPKLLIYNNRPSGV	60		
QY	233	PDRSGSGSGTSASLAIITGLQAEDEADYCCSYDSSLGSVFGGCTKYTVL	283		
DB	61	PDRSGSGSGTSASLAIISGLQSEDEADYCAAMDSDLDGYVFGCTKYTVL	111		
RESULT 18					
QY	173	OSVLTOPPSVSGAGGAGORVYTCISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDDSNRPSGV	232		
DB	1	OSVLTOPPSAGTGGGRTVTCISGSSSNVGSNZPRAYWYQOLPGTAPKLLIYNNRPSGV	60		
QY	233	PDRSGSGSGTSASLAIITGLQAEDEADYCCSYDSSLGSVFGGCTKYTVL	283		
DB	61	PDRSGSGSGTSASLAIISGLQSEDEADYCAAMDSDLDGYVFGCTKYTVL	111		
RESULT 19					
QY	173	OSVLTOPPSVSGAGGAGORVYTCISCTGRSSNIGAGHDVHWYQOLPGTAPKLLIYDDSNRPSGV	232		

	Ig heavy chain V-II region GAL
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=75059123; PubMed=4803843;
RA	Matanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT	The primary structure of a monoclonal IgM-immunoglobulin
RL	(macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT	type), subgroup B III. Architecture of the complete IgM-molecule.";
RL	Hoepfe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN	{2}
RP	REVISION TO 28-33.
RA	Hiltschmann N.;
RL	Submitted (JUN-1975) to the PIR data bank.
CC	-I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC	MACROGLOBULIN.
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	PIR: A02064; M3H0GL.
DR	HSSP: P01772; 2PB4.
DR	GO: GO:0005576; C:extracellular; NAS.
DR	GO: GO:0003823; F:antigen binding activity; NAS.
DR	GO: GO:0006955; P:immune response; NAS.
DR	InterPro: IPR007110; Ig-like.
DR	InterPro: IPR003506; Ig_MHC.
DR	InterPro: IPR003596; Ig_V.
DR	Pfam: PF00047; Ig_1.
DR	SMART: SM00406; IGv_1.
DR	PROSITE: PSS0835; IG_Like; 1.
KW	Immunoglobulin V region.
FT	DOMAIN 1 112 IG-LIKE.
FT	NON_TER 116 116
SO	SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;
<hr/>	
Query Match	26.8%; Score 439; DB 1; Length 116;
.Best Local Similarity	72.9%; Pred. No. 1,8e-25;
Matches 86; Conservative 11; Mismatches 19; Indels 2; Gaps	
DY	40 OVVLVSGGGGVOPGRSLRLSCASGFIFESYGMMHWROAPKGLGMVAGIFDGNKYK 99 ::: ::
Db	1 EVLVSEGGDLVDPGRSRLRISCSAAFGFBFBLMTVRQAPKGLEMLVANIKRBGSZBR 60
DY	100 ADVSKGRFTISRDNKNNTLYLQNNLSLAEDTAVYCARRGYYMDVMGKTGYTVSS 157 ::
Db	61 VDVSXGRFTISRDKAKNSLYLKQNLSLRVEDTLALYC-A-RGWGGDYWGCGLTIVYST 116
<hr/>	
RESULT 11	
HVF-HUMAN	
ID	SV3E_HUMAN STANDARD; PRT; 115 AA.
AC	P01767;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Ig heavy chain V-II region BUT.
OS	Homo sapiens (Human).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=78137069; PubMed=416441;
RA	Torano A., Putnam F.W.;
RT	*Complete amino acid sequence of the alpha 2 heavy chain of a human
RT	Igalpha immunoglobulin of the Azm (2) allotype."
RL	Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC	-I- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, AZM(2) ALLOTYPIC, C
CC	REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR:	A02050; A2HUBU.
HSSP:	P01789; IMCP.

DR GO:0005576; C:extracellular; NAS.
 DR GO:0003823; F:antigen binding activity; NAS.
 DR GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-Like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 DR PROSITE: PS0835; IG-LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 111
 FT NON_TER 115 115 IG-LIKE.
 SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCE4 CRC64;
 Query Match 26.3%; Score 431.5; DB 1; Length 115;
 Best Local Similarity 71.2%; Pred. No. 6.3e-25;
 Matches 84; Conservative 15; Mismatches 16; Indels 3; Gaps 2;
 QY 40 QVQLVQSGGVSVPGRSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAGIFYDGANKYY 99
 DB 1 EVQLVETGGGLTQPGSLRLSCAASGFTVSBHSMVVRQAPGKALZMWSAI-YRGGTTY 59
 QY 100 ADVSVGRFTISRDNKNTLYLQMSLRADETAVYYCARDRGYNDYMGKGTYYSS 157
 DB 60 ADVSVGRFTISRDNKNTLYLQMSLRADETAVYYCARDLA--AARLFEGKGTYYSS 115
 RESULT 12
 HV3C_HUMAN
 ID HV3C_HUMAN STANDARD; PRT; 117 AA.
 AC P01764;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region VH26 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81101090; PubMed=6450418;
 RA Mathysens G., Rabbitts T.H.,
 RT "Structure and multiplicity of genes for the human immunoglobulin
 heavy chain variable region."
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC -----
 CC
 DR EMBL: J00236; AAA53516.1; -
 DR EMBL: M35415; AAA58735.1; -
 DR PIR: A02047; H3H026.
 DR PDB: 1HOU; 23-DEC-99.
 DR Genew; HGNC:5545; IGHV6.
 DR GO:0005576; C:extracellular; NAS.
 DR GO:0003823; F:antigen binding activity; NAS.
 DR GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-Like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 DR PROSITE: PS0835; IG-LIKE; 1.
 DR Immunoglobulin V region; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-II REGION VH26.

FT DOMAIN 20 >117 IG-LIKE.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3C80F1 CRC64;
 Query Match 26.2%; Score 429; DB 1; Length 117;
 Best Local Similarity 82.7%; Pred. No. 9.7e-25;
 Matches 81; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 QY 40 QVQLVQSGGVSVPGRSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAGIFYDGANKYY 99
 DB 20 EVQLLESQGLVQPGSLRLSCAASGFTFSSYAMSVVRQAPGKLEWVSAISGSGSTYY 79
 QY 100 ADVSVGRFTISRDNKNTLYLQMSLRADETAVYYCAR 137
 DB 80 GDSVGRFTISRDNKNTLYLQMSLRADETAVYYCAK 117
 RESULT 13
 LV1C_HUMAN
 ID LV1C_HUMAN STANDARD; PRT; 111 AA.
 AC P01701;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-I region NEW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=69060892; PubMed=4177823;
 RA Langer B., Steinmetz-Kayne M., Hilschmann N.;
 RT "The complete amino acid sequence of Bence Jones protein New (lambda-
 type). Subgroups in the variable part of immunoglobulin L-chains of
 the lambda-type."
 RL Hoppe-Seyler's Z. Physiol. Chem. 349:945-951(1968).
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR: A01964; LIH0NW.
 DR HSSP: P01703; 7FAB.
 DR GO:0005576; C:extracellular; NAS.
 DR GO:0003823; F:antigen binding activity; NAS.
 DR GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-Like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 DR PROSITE: PS0835; IG-LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein;
 KW Pyroglutamate carboxylic acid.
 FT DOMAIN 1 105
 FT MOD_RES 1 1
 FT DISULFID 22 89
 FT NON_TER 111 111
 FT BY SIMILARITY.
 SQ SEQUENCE 111 AA; 11453 MW; AABCBCA3C49F2AD3 CRC64;
 Query Match 26.1%; Score 427.5; DB 1; Length 111;
 Best Local Similarity 73.2%; Pred. No. 1.2e-24;
 Matches 82; Conservative 13; Mismatches 16; Indels 1; Gaps 1;
 QY 173 QSVLTQPPSVSGAPQGVRTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGV 232
 DB 1 QSVLTQPPSVSAAPQGVRTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGI 59
 QY 233 PDRFSGSRGTSASLAITGLQAEADADYICQGYDSLSKGSVGGTGYVLG 284
 DB 60 PDRISASKSGTSATIGITGLRTGDEADYVCAATWDSLNAVVFVGSTKYTVLG 111
 RESULT 14
 LV1F_HUMAN

ID LV1F_HUMAN STANDARD: PRT: 109 AA.
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1989 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83221661; PubMed=6407018;
RA Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
RT "Complete covalent structure of a human immunoglobulin D: sequence of
RT the lambda light chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
DR HSSP: P01703; 7FAB.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig-MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 97 V SEGMENT.
FT DOMAIN 98 109 J SEGMENT.
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match 26.0%; Score 426.5; DB 1; Length 109;
Best Local Similarity 76.6%; Pred. No. 1.4e-24;
Matches 85; Conservative 10; Mismatches 13; Indels 3; Gaps 2;

OY 173 QSVLTQPPSVGARGQRTICTGRSSNIGAGHDYHWYQQLPGTPAKLLIYDDSNRPSGV 232
DB 1 QSVLTQPPSVGARGQRTICTGRSSNIGAGHDYHWYQQLPGTPAKLLIYDDSNRPSGV 59
OY 233 PDRFSGSRGTASALATGIAEDADYCCSYDSSLRGVFGGTGTVL 283
DB 60 PDRFSGSRGTASALATGIAEDADYCCSYDSSLRGVFGGTGTVL 108

RESULT 15

HV3E_HUMAN STANDARD: PRT: 120 AA.
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77117674; PubMed=65324;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monocytic IgM lambda and IgG kappa from an
RT individual patient. III. The complete amino acid sequence of the VH
RT region of the IgM paraprotein.";
RL Immunohistochemistry 13:995-999(1976).
CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE
CC SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
CC TYPE.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR: A02049; M3HUBW.

DR HSSP: P01772; 2FBA.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig-MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA: 13227 MW; D3F0428F7C2E6410 CRC64;

Query Match 26.0%; Score 426.5; DB 1; Length 120;
Best Local Similarity 70.8%; Pred. No. 1.5e-24;
Matches 85; Conservative 10; Mismatches 16; Indels 9; Gaps 2;

OY 40 QVQLVQSGGAVYVPGSRSLRSCAASGFTFSSYGMHWYQAPGKGLDWAGIFYDGKRY 99
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYNNMWYQVYRGKGLDWYSAT-GTAGDOY 59
OY 100 ADSYKGRPTISRDNKNTLYIQMNSLRADTAIVYYCARD-----RGYYMDYWGKGT 151
DB 60 ADSYKGRPTISRDNKNTLYIQMNSLRADTAIVYYCARDSPVSLVDGMLYYYYGSGVWGQGT 119

Search completed: September 22, 2003, 15:13:49
Job time : 12.6541 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:13:04 ; Search time 50.6122 Seconds
(without alignments)
1580.572 Million cell updates/second

Title: US-10-052-798-11

Sequence: 1 MTMTTPSGAFFLEIFNVK.....HHGGAEQKLISEEDLNGAA 31C

Scoring table:

Gapor 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
```

Database :

```

1:  sp.archaea:*
2:  sp.bacteria:*
3:  sp.fungi:*
4:  sp.human:*
5:  sp.invertebrate:*
6:  sp.mammal:*
7:  sp.mhc:*
8:  sp.organelle:*
9:  sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	891	54.4	298	11	Q9XYFO	Q9XYFO mus musculi
2	606.5	37.0	241	11	Q92LI6	Q92LI6 mus musculi
3	546	33.3	613	4	Q8WUK1	Q8WUK1 mus sapien
4	544	33.2	218	11	Q925S1	Q925S1 mus musculi
5	538.5	32.9	237	4	Q8WUK4	Q8WUK4 homo sapien
6	532.5	32.5	237	4	Q8WUT6	Q8WUT6 homo sapien
7	521.5	31.8	113	4	Q9UL90	Q9UL90 homo sapien
8	508	31.0	236	4	Q9UE61	Q9UE61 homo sapien
9	504.5	30.8	116	4	Q9UL93	Q9UL93 homo sapien
10	502	30.6	573	4	Q8WU38	Q8WU38 homo sapien
11	493	30.1	147	4	Q9Y509	Q9Y509 homo sapien
12	490	29.9	122	4	Q9UL84	Q9UL84 homo sapien
13	483	29.5	471	4	Q8WC77	Q8WC77 homo sapien
14	482.5	29.5	597	4	Q9GBB9	Q9GBB9 homo sapien
15	475.5	29.0	121	4	Q9UL71	Q9UL71 homo sapien
16	475	29.0	499	4	Q8NSK4	Q8NSK4 homo sapien

17	465	28.4	493	4	08NC16	08nc16	homo	sapient
18	464	28.3	112	4	09HC1	09hc1	homo	sapient
19	463	28.3	118	4	09UL72	09ul72	homo	sapient
20	457	27.9	118	11	091205	091205	mus	sapient
21	453	27.7	118	4	09UL91	09ul91	homo	sapient
22	444.5	27.1	487	11	099Kx4	099kx4	mus	sapient
23	441.5	27.0	479	11	091W5	091w5	mus	sapient
24	436.5	26.6	110	4	08TE63	08te63	homo	sapient
25	434	26.5	236	4	08NEJ1	08nej1	homo	sapient
26	430.5	26.3	494	4	09K6K8	09k6k8	homo	sapient
27	425	25.9	486	11	091Z07	091z07	mus	sapient
28	421.5	25.7	119	11	0920E7	0920e7	mus	sapient
29	421.5	25.7	480	11	091XE1	091xe1	mus	sapient
30	418	25.5	95	4	09ULB6	09ulb6	homo	sapient
31	416.5	25.4	469	11	08RL39	08rl39	mus	sapient
32	409	25.0	484	11	08VE0	08ve0	mus	sapient
33	401.5	24.5	521	4	08N4Y9	08n4y9	homo	sapient
34	400.5	24.5	108	4	096S80	096s80	homo	sapient
35	393.5	24.0	170	11	092552	092552	mus	sapient
36	393.5	24.0	437	11	09R1A4	09r1a4	mus	sapient
37	393.5	24.0	484	11	099L16	099l16	mus	sapient
38	391	23.9	124	6	09N0M4	09n0m4	oryzotolagus	
39	388	23.7	124	6	09N0M6	09n0m6	oryzotolagus	
40	385.5	23.5	131	4	09UL88	09ul88	homo	sapient
41	384.5	23.5	101	4	081ZD8	081zd8	homo	sapient
42	377.5	23.0	104	4	09UL87	09ul87	homo	sapient
43	374.5	22.9	500	4	09BRV0	09brv0	homo	sapient
44	371	22.6	159	4	096O50	096o50	homo	sapient
45	369.5	22.6	116	4	096JDO	096jdo	homo	sapient

ALIGNMENTS

RESULT 1	
09QYF0	
ID	09QYF0 PRELIMINARY; PRT; 298 AA.
AC	09QYF0;
DT	01-MAY-2000 (Tremblrel. 13, Created)
DT	01-MAY-2000 (Tremblrel. 13, last sequence update)
DT	01-MAR-2003 (Tremblrel. 23, last annotation update)
DE	CN 8 scFv.
GN	CN 8.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-Balb/c; TISSUE-Spleen;
RX	MEDLINE=20183931; PubMed=10706631;
RA	Shinozawa N., Demura T., Fukuda H.;
RT	"Isolation of a vascular cell wall-specific monoclonal antibody
RT	recognizing a cell polarity by using a phage display subtraction
RT	method."
RL	Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR	EMBL: AB036341; BAA8633.1; -.
DR	HSSP: P01607; IREI.
DR	InterPro: IPR007110; Ig-like.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_V.
DR	Pfam: PF00047; Ig; 2.
DR	SMART: SM00406; IGV; 2.
DR	PROSITE: PSS0835; IG_LIKE; 2.
SO	SEQUENCE 298 AA; 31867 MW; E0F96BBA17004317 CRC64;
Query Match	54.48; Score 891; DB 11; Length 298;
Best Local Similarity	64.08; Pred. No. 3; 3e-59;
Matches 185; Conservative 29; Mismatches 67; Indels 8; Gaps	
1	MTMTTSPGCAFLIEIFRVKKLLFAIPLVYPFYAQAAMQVLYSGGSGVPGKSLRLS 60
1	MTMTTSPGCAFLIEIFRVKKLLFAIPLVYPFYAQAAMQVLYSGGSGVPGKSLRLS 60

AC	Q9UL90;	PRELIMINARY;	PR1;	113 AA.
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	Myosin-reactive Immunoglobulin heavy chain variable region (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98277139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,			
RA	Young D.C.;			
RT	Myosin-reactive autoantibodies in rheumatic carditis and normal			
RT	fetus.";			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR	EMBL; AF035024; AAD56260.1; -.			
DR	HSSP; P01772; 2F8A.			
DR	Interpro; IPR007110; I9-1like.			
DR	Interpro; IPR003006; IG_MHC.			
DR	Interpro; IPR003596; I9_v.			
DR	Efam; PF00047; I9; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG-LIKE; 1.			
FT	NON_TER	1	1	
FT	NON_TER	113	113	
SQ	SEQUENCE	113 AA;	12437 MW;	ED57FDD19086D07F CFC64;

```

Query Match      31.8%; Score 521.5; DB 4; Length 113;
Best Local Similarity 85.6%; Pred. No. 5.9e-32;
Matches 101; Conservative 4; Mismatches 8; Indels 5; Gaps 1;

QY 40 QVQLVSGGGVQPGGSLRLSCAASGFTFSYSGMHVWRQAPGKGLMVAIFPDGNGKYY 99
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 1 EVQLVSGGGVQPGGSLRLSCAASGFTFSYSGMHVWRQAPGKGLMVAIFIRYDSNKKY 60

QY 100 ADSVKGRTISRDNKNTLYLQMSLRADFTAVYCARPGYKXNDVWGKGTIVYSS 157
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ADSVKGRTISRDNKNTLYLQMSLRADFTAVYCARGLDNTY-----WGQGLTVYSS 113

RESULT 8
ID 096E61 PRELIMINARY; PRT; 236 AA.
AC 096E61;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBL_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012876; AAH12876.1; -
DR InterPro; IPR007110; I9_1like.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_V.
DR Pfam; PF00047; I9_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IGV_LIKE; 2.
DR PROSITE; PS00290; IGV_MHC; 1.
KW Hypothetical protein.
SQ
SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match      31.0%; Score 508; DB 4; Length 236;
Best Local Similarity 83.6%; Pred. No. 1.5e-30;
Matches 97; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 169 GGSQSGLTQPPSVSGAPGQRYTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDSDNR 228
   | : ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
DB 16 GSAQSVLAPPSVSAPGQYTIISCTGSTINGAGYAVHWYQPGAPKVLITGNKRR 75

QY 229 PGVDPDRFSGNSGTSASLAITGLQAEADADYVCGSYDSSLKSGVFSGTKYTVLG 284
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 76 PGVDPDRFSGNSGTSASLAITGLQAEADADYVCGSYDSSLKSGVFSGTKYTVLG 131

RESULT 9
ID 09UL93 PRELIMINARY; PRT; 116 AA.
AC 09UL93;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBL_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-9827139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
   Young D.C.;

```

```

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -
DR HSSP; P01772; 2F84.
DR InterPro; IPR007110; I9_1like.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_V.
DR Pfam; PF00047; I9_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IGV_LIKE; 1.
FT NON_TER 1 116
FT NON_TER 1 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match      30.8%; Score 504.5; DB 4; Length 116;
Best Local Similarity 84.6%; Pred. No. 1.1e-30;
Matches 99; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 41 VOLVSGGGVQPGGSLRLSCAASGFTFSYSGMHVWRQAPGKGLMVAIFPDGNGKYYA 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 VOLVESGGGVQPGGSLRLSCAASGFTFSYSGMHVWRQAPGKGLMVAIVSYDGSNKYYA 60

QY 101 DSVKGRFTISRDNKNTLYLQMSLRADFTAVYCARPGYKXNDVWGKGTIVYSS 157
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 DSVKGRFTISRDNKNTLYLQMSLRADFTAVYCARPGYKXNDVWGKGTIVYSS 116

RESULT 10
ID 08WU38 PRELIMINARY; PRT; 573 AA.
AC 08WU38;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBL_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Tonsil;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021276; AAH21276.1; -
DR InterPro; IPR007110; I9_1like.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_V.
DR Pfam; PF00047; I9_4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IGV_LIKE; 2.
DR PROSITE; PS00290; IGV_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match      30.6%; Score 502; DB 4; Length 573;
Best Local Similarity 42.4%; Pred. No. 1.2e-29;
Matches 131; Conservative 28; Mismatches 72; Indels 78; Gaps 12;

QY 40 QVQLVSGGGVQPGGSLRLSCAASGFTFSYSGMHVWRQAPGKGLMVAIFPDGNGKYY 99
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 20 EVQLVSGGGVQPGGSLRLSCAASGFTFDDYAMHWWRQAPGKGLMVAISWNSGSGY 79

QY 100 ADSVKGRTISRDNKNTLYLQMSLRADFTAVYCARPDR-----GYYY-KDVWGKGTIV 153
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 ADSVKGRTISRDNKNTLYLQMSLRADFTALYICAKHGSSYIGYIGMVGKGTIV 139

QY 154 TVSSGGGGSGGGSGGGGQSVLTQPPSV-----SGA-----PGQRYTISC--TGRSSNIGA 203
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 140 TVSSAP-----TKAPDVFPITISGGRHPKDNQSPVLAACLTIGYHP---T 179

QY 204 GHDVHWY-----QQLPGTAPKLLIYDSDNRPSPGVPPDRFSGNSGTSASLAITGLQAEAD 259

```

```

DB 180 SVYTWYMGTOQOPORTPEIORRD-----SYMTSSQSL-TPLOQWRGE 224
QY 260 YVC--QSYDSSLRGSVF-----GGGKRVYVGLAAHHHHHNGA 296
DB 225 KCVVQHTPASKKEIFFWPESPKAQASSVPTAOPQAEGLAKATTAATPTNTGRGGE 284
QY 297 EOKLISEED 305
DB 285 KKKEKEKE 293

RESULT 11
QY509 PRELIMINARY: PRT; 147 AA.
AC 09Y509;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE VH3 Protein (Fragment).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL: S80860; A014339.1; -
DR HSP; P01772; 2EB4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER
FT SEQUENCE 147 AA; 15768 MW; 8489FCAAT7BC925C CRC64;

Query Match
Best Local Similarity 64.0%; Score 493; DB 4; Length 147;
Matches 103; Conservative 10; Mismatches 22; Indels 26; Gaps 4;

QY 40 QVOLVQSGGVVQPGKSLRLSCAASGFIFSSYGMHVRQAPGKLEWAGIFYDGKNTY 99
DB 1 QVHLVESGGGVVQPGKSLRLSCAASGFTFTSYGMHVRQAPGKGLDVALISTDSTQY 60
QY 100 ADVKGRFTISRDNSKNTLYIQMNSLRADTAVYYCARDR-----GYYY--MDVWGKGT 151
DB 61 ACSVAGRFTISRDNSKNTLYIQMNSLRVEDTAVYYCAKNGYFDSYGYAGIDWGGQT 120
QY 152 TTTVSSGGGGSGGGSGGSVLTQPPSVSG-APGQVY 191
DB 121 LVTVSSAS-----TKGVSVEPLAPSSKST 144

RESULT 12
QY509 PRELIMINARY: PRT; 122 AA.
AC 09UL84;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035030; A045626.1; -
DR HSP; P01772; 2EB4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER
FT SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match
Best Local Similarity 29.9%; Score 490; DB 4; Length 122;
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 2;

QY 40 QVOLVQSGGVVQPGKSLRLSCAASGFIFSSYGMHVRQAPGKLEWAGIFYDGKNTY 99
DB 1 EVQLVESGGGVVQPGKSLRLSCAASGFTFTSYGMHVRQAPGKLEWVAISNDGSKTY 60
QY 100 ADVKGRFTISRDNSKNTLYIQMNSLRADTAVYYCARD-RGY--YMDVWGKGTTVY 155
DB 61 ADVKGRFTISRDNSKNTLYIQMNSLRADTAVYYCAKDERRLVGTGYDYGQGLTVY 120
QY 156 SS 157
DB 121 SS 122

RESULT 13
QY509 PRELIMINARY: PRT; 471 AA.
AC 08TC77;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical Protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC024289; AAH24289.1; -
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_4.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical Protein.
FT SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match
Best Local Similarity 29.5%; Score 483; DB 4; Length 471;
Matches 97; Conservative 13; Mismatches 35; Indels 14; Gaps 2;

QY 40 QVOLVQSGGVVQPGKSLRLSCAASGFIFSSYGMHVRQAPGKLEWAGIFYDGKNTY 99
DB 20 EVQLVESGGGVVQPGKSLRLSCAASGFTFTSYGMHVRQAPGKLEWVSSMSSTIY 79

```

